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-Q=/cgn2_1/USPTO_spool/BORIN682/runat_23012003_130141_7873/app_query.fasta_1.597
-Q=/cgn2_1/USPTO_spool/BORIN682/runat_23012003_130141_7873/app_query.fasta_1.597
-DB=GenEmbl -QFWT-fastap -SUFFIX-colip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-blts -START=1 -END=-1 -MATRIX=011go -TRANS-human40.cdi -LIST=1000
-UNITS-blts -START=1 -END=-1 -MATIX=011go -TRANS-human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE-LOCAL -OUTFMT=pto
-NORM-ext -HEAPSIZE=500 -MINLEN=2000000000
-USER-BORIN682_eCGN_11_2425_erunat_23012003_130141_7873 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NGE_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. ဂ ဂ C ဂ ဂ 0000 000000 Score Query Match 1000 10000 1 777 934 11434 11434 174342 771 155416 174342 771 155416 775 185237 3014 4011 9963 36021 72519 81292 83292 83292 83292 83292 83292 108460 105756 107637 108461 108661 1087637 Length B ωνουνουνουνουνουνουνουνουνουωνουνουνουνουνου 10 A04913 A04915 ENSLIPPA ENSLIPPA ENSLIPPA ENSLIPPA ENSLIPPA ECOTOXA E03421 S60731 AB011677 A16419 AB011897 ECCELTA E006133 ACC101336 AE013887 ACC111766 AE013887 ACC111766 AE011897 ACC111769 ACC111691 ACC121499 ACC121697 ACC113697 ACC113996 ACC128996 EWDLTA AF242417 P307LTA M57244 Plasmid EWD AF242417 Escherich M35581 Plasmid p30 A04913 E.coli LTA A04913 E.coli LTA A04915 Artificial M15362 Plasmid ENT M15361 Plasmid ENT M15362 Plasmid ENT M15362 Sequence E00613 DMA encodin AC114463 Rattus no AC114463 Rattus no BC021349 Mus muscu BC021349 Mus muscu BC024766 Mus muscu U10336 Helobdella AE013887 Yersinia AE013887 Yersinia AC004462 Homo sapi AC130257 Rattus no AC112166 Rattus no AC121484 Rattus no AC113697 Rattus no AC113697 Rattus no AC103598 Rattus no AC107589 Rattus no AC107589 Rattus no AC107589 Rattus no AC1026736 Homo sapien AC128996 Rattus no AC1026736 Homo sapien AC128918 Rattus no AC103101 Rattus no AC103101 Rattus no AC103101 Rattus no AC103130 Rattus no AC103131 Rattus no AC103131 Rattus no AC103134 Rattus no AC115134 Rattus no AC155871 Human DNA AC115144 Rattus no AC155871 Human DNA AC115144 Rattus no AC155871 Human DNA AC115144 Rattus no AC155871 Human DNA AC1155871 Human DNA Description

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Plasmid P307
Plasmid P307
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                                                                                                                                                                                                                                                                                                                                                                                                                            p307LTA 777 bp DNA plasmid P307 (from E.coli) heat-labile gene, complete cds.
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REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDTCN
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subunit A (lta)
RESULT
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RESULT 3 P307LTA

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SEQ1-65TO79 (1-15) x P307LTA (1-777)
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Hayes, M.V., Harford, S. and Ross, G.W.
Microbiological process
Patent: EP 0145486-A 5 19-JUN-1985;
GLAXO GROUP LIMITED
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Escherichia coli
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EETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL"
a 136 c 164 g 222 t
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136 C 164 g 222 t
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IYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRN
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Plasmid ENT P307 (enterotoxigenic
M15362
M15362.1 GI:148337
LTp gene; heat-labile toxin.
Plasmid ENT (enterotoxigenic E.col
                                                                                                                                                                                                                                                       p370.
Plasmid ENT
                                                                                                                                                                       Yamamoto, T., Gojobori, T. and Yokota, T.
Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae 01
J. Bacteriol. 169 (3), 1352-1357 (1987)
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A04915
A04915.1 GI:412519
                                                                                                                      Clean copy of sequence [1] kindly (22-APR-1987).
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Patent: EP 0145486-A 7 19-JUN-1985;
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1 (bases 1 to 777)

Hayes, M.V., Harford, S. and Ross, G.W.
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135 c 164 g 222 t 1 others
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               /codon_start=1
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Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae Ol
J. Bacteriol. 169 (3), 1352-1357 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M15361
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                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
/protein_id="AaA24791.1"
/protein_id="AaA24791.1"
/db_xref="G1:148334"
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/translation="MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRSGYSTYY
HNEYEDRGTONNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQSILDERLHRN
IYIATAPNMFNYNDVLGVYSPHPYEQEVSALGGIPYSQIYGMYRVNFGYIDERLHRN
IYIATAPNMFNYNDVLGVYSPHPYEQEVSALGGIPYSQIYGMYRNFGYIDERCHRN
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Plasmid ENTR"
/db_xref="taxon:2462"
/plasmid="Plasmid ENTR"
122. .898
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Hneyepgrgrounur/ghargrgtgryryddgvstsleslasalggsilsgrstyr
Iyviatapmynunur/grysphpyabevsalggifyrgyryrgyrupgytdeklhr
Reyrdryyrnuniapaedgyrlagfppdhqawreepwihhapqgcgnssrtitgdtcn
                                                                                /product="Heat labile
155 c 186 g
                                                                                                                            /note="Heat labile toxin subunit A signal 176. .895
                                                                                                                                                                                       REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITGDTCN
EETQNLSTIYLREYQSKYKRQIFSDYQSEVDIYNRIRDEL"
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                                                                                                                                                                                                                                                                                                                                                                              /note="Heat labile toxin subunit A precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/db_xref="GI:148338"
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E.coli Hinan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, T., Tamura, T. and Yokota, T. Yamamoto, T. Tamura, T. and Yokota, T. Primary structure of heat-labile enterotoxin Escherichia coli pathogenic for humans
J. Biol. Chem. 259 (8), 5037-5044 (1984)
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212. .787
/product="heat-labile enterotoxin A1"
794. .931
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REYRDRYYRNLNIAFAEDGYRLAGFPPDHQAMREEDMIHHAPQGCGDSSRTITGDTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Escherichia
/db_xref="taxon:562"
158. .934
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165 c 186 g 285 t
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KITASATO INST:THE

OS ESCHETICHIA COLI

DN JP 1992079898-A/1

PN JP 1992079898-A/1

PD 13-MAR-1992

PF 23-JUL-1990 JP 1990194:

PI DANBARA HIROFUMI, ABE;

PC C1201/68,C07H21/02,C07;

PC (1201/58,C07H21/02,C07;

PC (1201/5/31,C12R1:19),(()

PC (1201/5/31,C12R1:19),(()

Strandedness: Double;

CC 10001099: Linear;

CC hypothetical: No;

CC anti-sense: No;

CC anti-sense: No;

CC anti-sense: No;

CC anti-sense: No;

CC Apported to the colore of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
FT mat_pep
FT CDS
FT CDS
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DNA encoding LTh of entero toxigenic Escherichia coli.
E03421
E03421.1 GI:2171637
JP 1992079898-A/1.
Escherichia ----
s60731 1275 bp DNA linear BCT 29-heat-labile enterotoxin A subunit, heat-labile enterotoxin subunit [Escherichia coli, 21d, Genomic, 1275 nt].
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Danbara, H. and Abe, A.
DANBARA, H. and Abe, A.
DNA AND RNA PROBE TO SIMULTANEOUSLY DETECT VIBRIO CHOLERATE AND
ENTEROTOXIGENIC ESCHERICHIA COLI AND DETECTION OF VIBRIO CHOLERA
AND ENTEROGEXIGENIC ESCHERICHIA COLI USING THE SAME DNA AND RNA
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Bacteria; Proteobacteria;
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DANBARA HIROFUMI, ABE AKIO
C1201/68,C07H21/02,C07H21/04,C12N15/11,C12N15/31,C12Q1/04,
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*source: clone=pKAD008;
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/db_xref="taxon:562"
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RESULT 11
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AB011677
                    heat-labile enterotoxin B subunit; LTh b subunit; heat-labile enterotoxin A subunit; LTh a subunit. Escherichia coli (strain:1032 (Enterotoxigenic)) DNA.
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Location/Qualifiers
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Escherichia
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Escherichia coli
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publication: LTC A subunit"
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/protein_id="AAC60440.2"
/protein_id="AAC60440.2"
/db_xref="Gi:18390349"
/translation="MKNITFIFFILLASPLYANGDKLYRADSRPPDEIKRSGGLMPRG
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/translation="MKNITFIFFILLASPLYANGDKLYRADSRPPDEIKRSGGLMPRG
/translation="MKNITFIFFILLASPLYANGDKLYRADSRPPDEIKRSGSTLSGGSTSYY
/translation="MKNITFIFFILLASPLYANGDKYSTSLLSRRPPDEIKRSGSTLSGGSTSYY
/translation="MKNITFIFFICTORY RYDDGY VATURGIFT GUTCHPRG
/translation="MKNITFIEL"
/translation="M
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ILSYTESMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="heat-labile enterotoxin B subunit"
/protein_id="AAC60441.1"
/db_xref="GI:408996"
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/db_xref="taxon:562"
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RESULT 12
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AUTHORS
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Best Local Similarity:
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Escherichia coli heat-labile enterotoxin with a trace amount of the holotoxin as a influence amount of the holotoxin as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (07-MAR-1998) Katsuhiro Komase, The Kitasato Institute, Center for Basic Research, Lab. of Virology; Shirokane 5-9-1, Minato-ku, Tokyo 108-8642, Japan (E-mail:komase-k@kitasato.or.jp, Tel:+81-3-3444-6161, Fax;+81-3-3444-6637)
              A16419.1
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91. .867
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/protein_id="BAA25725.1"
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HNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQSILSGYSTYY
                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MMKVKCYVLFTALLSSLCAYGAPQSITELCSEYRNTQIYTINDK
ILSYESMAGKREMVITTFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETK
IDKLCVWNNKTPNSIAAISMEN"
258 c 286 g 402 t
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REYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGNSSRTITDDTCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="heat-labile enterotoxin
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864. .1238
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/codon_start=1
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/strain="1032 (Enterotoxigenic)"
/db_xref="taxon:562"
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K., Suzuki,Y., Nagamine,T.,
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1 SerLeuArgSerAlaHisLeuAlaGlyGln
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AR118597
                                                                                                                                                                                                          Domenighini,M., Rappuoli,R., Pizza,M. and Hol,W. Immunogenic detoxified mutants of cholera toxin and of the LT, their preparation and their use for the preparation of Patent: US 6149919-A 5 21-NOV-2000;
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Escherichia coli
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/db_xref="GI:641009"
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HPYEGEVSALGGIPSOIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRL
AGFPPDHQAMREEPWHHAPQGCGDSSRTITGDTCNEETQNLSTIYLREYQSKVKRQI
FSDYOSEVDIYNRIRDEL"
                                                                                                                                                                 /organism="unknown"
123 c 156 g
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/db_xref="taxon:562"
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                               REFERENCE
AUTHORS
TITLE
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SEQ1-65TO79 (1-15) x ECELTA (1-868)
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Patent: JP 1986005097-
GLAXO GROUP LTD
OS Escherichia coli
PN JP 1986005097-A/1
                                                                   Escherichia.

1 (bases 1 to 777)

MAINURUM, H., Suteilbun, H. and Goodon, U.R.
MICROBIAL METHOD
                                                                                                                                         Escherichia coli.
Escherichia coli
Bacteria; Proteobacteria;
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JP 1986005097-A/1.
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J. Biol. Chem. 257 (10), 5716-5721 (1982)
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V00275 J01604
V00275.1 GI:41339
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                                                   JP 1986005097-A 1 10-JAN-1986;
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/db_xref="GI:41340":P06717"
/db_xref="SWISS-PROT:P06717"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGDSSRTITGDTCNEETQ
NLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mknitfiffillasplyangdrlyradsrppdeikrfrslmprg
NEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQYILSGYSLTIY
IVIANMFNVNDVISVYSPHFYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYR
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/db_xref="taxon:562"
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                                 Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C.C., Escotto, M., Fralls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
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hypothetical: No;
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GOODON UIRIAMU ROSU
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12-DEC-1983 GB 83 83331
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       Harris, K., Hart, M., Havlak, P.,
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       Hawes, A.,
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Hernandez,J.
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IN PROGRESS
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Direct Submission

Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 14, 2002 this sequence version replaced gi:19310258.
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Direct Submission
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                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 51 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
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Consensus quality: 115361 bases at least Q40
Consensus quality: 118379 bases at least Q30
Consensus quality: 122104 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
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Barbarla, J., Benton, J., Blange, K., Blankenburg, K., Bonnin, D., Bundey, K., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Carron, T.F., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferragutto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hartis, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Huber, J., Jackson, L.E.,
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***, 84 unordered pieces.
AC120067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/organism="Rattus norvegicus"
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       A., Hernandez,J.,
, Hollins,B.,
, Jackson,L.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-MAY-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA (bases 1 to 174342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 174342) Worley, K.C. Direct Submission
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On Jul 18, 20
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                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 84 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are unknown.

This record will be updated with the finished sequence
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Consensus quality: 111889 bases at least Q40
Consensus quality: 118225 bases at least Q30
Consensus quality: 122144 bases at least Q20
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Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
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Mus musculus, clone MGC:29285 IMAGE:3985822,
BC021349
                                                                                                                             Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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KEYWORDS
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Best Local Similarity:
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  Contact:
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                                                                  Direct Submission
Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General Can
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                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young,A., Zhang,L.-H. and Green,E.D.
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/protein_id="AAH21349.1"
/db_xref="G1:18204169"
/db_xref="G1:18204169"
/translation="MKKRDLEPSDATYTALFNVCAESPWKDSALGSALKLRQQLQARN
/translation="MKKRDLEPSDATYTALFNVCAESPWKDSALGSALKLRQQLQARN
FQLNLKTYHALLKVAAKCADLRLCLDVEKEIIQRCHAVSRTLLLTSQEENILLPPPK
RQAMQVWRQMLSIGIKPSRHGYNLLLEAARDGGLDEVASRLLLLTSQEENILLPPPK
RQAMGVWRQMLSIGIKPSKHYBALERQLFLEPSQKLEGPPALPEARVTSRTQPEVET
TAEPGHTVALTPLAPKPTHLELEVSLLSIGTLSPAVVSFGTVATPADRLALMGGLEGF
TAEPGHTVALTPLAPKPTHLELEVSLLSIGTLSPAVVSFGTVATPADRLALMGGLEGF
LGKMTEHGLQPDIKTLTILAEVVEPGSAAESSLLSVLDRRADMKKSQVSPNIHIY
STLINAALKKLDYTYLISILKDMRQNSVEVNEVVVRQLEEAAEYPFTFDRYKGKNTYL
EKIDGERAYYKQWLKAMPAEEAPHFWQEFQNKPVGDQDTTDKAGGLRDG"
EKIDGERAYYKQWLKAMPAEEAPHFWQEFQNKPVGDQDTTDKAGGLRDG"
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old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
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/note="Voot:
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/db_xref="taxon:10090"
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Helobdella stagnalis.
Helobdella stagnalis
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida;
Rhynchobdellida; Glossiphoniidae; Helobdella.
                                                                                                                                           partial cds.
U10336
                                                                                                                                                                                     Helobdella stagnalis RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 6 Row: o Column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
YOon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genom Sequencing Center
                                                                                                                    U10336.1
                                                                                                                                                                                                             HSU10336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              passed the following selection criteria: Hexamer frequency ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Similar to KIAA0632 protein"
/product="Similar to KIAA0632 protein"
/protein_id="AAH04766.1"
/db_xref="Gi:13435831"
/translation="MKKEDLEPSDATYTALFNVCAESPWKDSALQSALKLRQQLQARN
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RQAMQVWRQMLSIGIKFSRHGYNLLLEAARDCGLGDPEVARRLLLTSQEENILLPPRE
GRHMAGRKVQAKTVHGVSIRHVEALERQLFLEFSQKLEGPFALPEARVTSRTQPEVET
TAEPGHTYALTPLAPKCTHLELEVSLLSIGTLSPAVVSEGTVATPADRLALMGGLEGF
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STLINAALKKLDYTYLISILKDMRQNSVPVNEVVVRQLEFAAEYPPTFDRYKGKNTYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Mammary tumor. C3(1)-Tag mode
ductal carcinoma. 5 month old virgin mouse.
/clone_lip="NCI_CGAP_Mam6"
/lab_host="DH10B"
                                                                                                                    GI:520512
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/db_xref="taxon:10090"
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/tissue_type="Mammary tumor. C3(1)-Tag model.
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Best Local Similarity:
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95041334
Yersinia pestis KIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 4011)
Sidow, A. and Thomas, W.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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GNKINISOVIACVGQQONVEGKRIPFGFRORTLPHFIKDDYGPESERGFVENSYLAGLTP
TEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKAMESVMVKYDGTVRNQIEQLIQLNURY
GEDGLAGEMVEFQNLPSKAFERAGFKFDDTNEKHLKNYLDEDILKSLUGDANURY
AEVESEYKQLLEDRTAIRQIFPSGDSKIVLPCNLQRLIMNAQKIFRIHTRKPSNLHPV
KIIEDVRELSKKFMIVKGEDRLSKTANTNATLLMNILVRSTLCSKRVIEEFHLSTEAF
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AVNKMTRRDTFITKDEIMNILMYLPGWAGKLEQDAIIKRPALMYGKQLESIIIPGRIN
VIRYHSTHPDDEDRGPKMISPGDTKVLVEDGKLLSGIILCKKSLGASSGSLQHIIHME
LGSDATADFYAYIQMVTNHWLLVTGHTIGIADTIADAKTYSDIQTAIKKAKSDVVEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKŢKNOMKRROGFVYDLCKVETSCGGGEIDKKDDDNDPDNIKVOVGCGRHOPKIRRNL
LELTAŁEWKO INDDNOKKMILTAERVLEIFKA TDETCTILGMOPKYARDEVLIATML
PVPPLPVRPAVVMFCSAKNODDLTHKLADIIK INNOLKREMIGAAHILLAEDTKMLO
FHVATMIDNEMPGLPRATOKSGRPLKSIKORLKGKEGRIRGNLMGKRVDFSARTVITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLQGITSIAKYYMQQPTTDDKKRIIIDEKGEFKALQDWILETDGTALRRVLSVENVDP
VKTVSNDIVEVFEVLGIEAVRKSIEREMNNVISFDGSYVNYRHLALLCDVMTAKGHLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKEIINVSKKPRAPSLTVILIGQPARDAEKAKDVLCQLEHTTLRKVTENTAIYYDPDP
MHTLIEEDQEWVYIYYDMPDVDISRLSPWLLRVELDRKRMTDKKLTMEQISEKITAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt EWLMGEIESKFIQARVQPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPMLRIDQVGVPRSIAQNLTFPEIVTPFNIERLTELVKRGANQYPGAKFILRETGDRI
DLRYHPKSTDLHLQFGYRVERHMQDNDYVIFNRQPTLHKMSMMCHRVKILPWSTFRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="RNA polymerase II, largest subunit"
/protein_id="AAA50227.1"
/db_xref="Gi:520513"
/translation="HIELSKPVFHVPFFTKIIKILRCVCYYCSKLLIDPNHPKVKDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 degenerate oligos (external to the sequence shown) from first strand cDNA. See Reference 1 for details"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDDLNCIFNDDNAEKLVLRVRLMSNQDGKQDQDTEEQIDKMPDDTFLKHIESNMLTDM
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J. Bacteriol. 184 (16), 4601-4611 (2002)
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                                                                                                                                                                                                                                                                acids, amines"
/note="residues 10 to 252 of 252 are 78.60 pct identical to residues 1 to 243 of 243 from E. coli K12: B0860; residues 4 to 252 of 252 are 77.51 pct identical to residues 12 to 260 of 260 from GenPept: 9blAAG55239.1|AE0052674 (AE005267) arginine 3rd transport system periplasmic binding protein [Escherichia coli 0157:H7 EDL933]"
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of proteins, pepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of proteins, peptides, glyco"
/note="residues 12 to 271 of 308 are 25.00 pct identical
to residues 3 to 247 of 283 from GenPept :
>gblnAD36886.1lAE001819_9 (AE001819) ftsH protease
activity modulator HflC [Thermotoga maritima]"
/translation="mknsdrslsmkklllatllsgmafsataaetlrfaasatyppfe
smdaneivgfdmdlakalckomeanctftnoafdslifalkerkydavisgmbitpe
rskovaftdpyfansaivlapygkfsgtfadlkkigmengtthokvlodkhebigty
sydsygnaiidlkngridgvfgdtavvnewlktnpnlasvgehvtdpoxfgtglgiav
                                                                                                                                                          /product="arginine 3rd transport binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="1
1932. .
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LRRVLKDEPLIINSVNIENIDFTEGYEASIEERMKAEVNVEKTRKMLETEKINADIAI
EQARGQSESQLSIAKIGAEKIKLMGAAEAENIRLMGAAEAEKIKLRADALKQNPLLVE
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/protein_id="AAM86394.1"
/db_xref="GI:21959740"
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/gene="hflc"
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/note="y2843"
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                                                                                                          /protein_id="AAM86395.1"
/db_xref="GI:21959741"
                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="transport; transport of small molecules; amino
acids, amines"
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Schwartz, D.C.,
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Schwartz, D.C.,
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complement(2817.
/gene="y2845"
complement(2817.
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/gene-"y2846"
/gene-"(4031. .4495)
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/function="putative"
/note="residues 1 to 372 of 375 from E. coli K12: B0859;
residues 1 to 372 of 375 from E. coli K12: B0859;
residues 1 to 372 of 376 are 75.53 pct identical to
residues 1 to 372 of 375 from GenPept:
-ygb|AAG55235.1|AE005266_14 (AE005266) putative enzyme
[Escherichia coli 0157:H7 EDL933]"
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/gene="potI"
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acids, amines"
/note="residues 18 to 318 of 321 are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="munipevrsywrrviltvgytflyapmlmlviysfnssklytvwagmstrwytqlfndsamisavglsltiaaasatmavvlgtiaavvmvrfgrfrgstgfafmltaplynpdvitglsllllfvamghaigwfaergmftimlahvtfctayvtvvis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="residues 1 to 280 of 281 are 84.28 pct identical to residues 1 to 280 of 281 from E. coll K12: 80857; residues 1 to 280 of 281 are 85.00 pct identical to residues 1 to 280 of 281 from GenPept: >gb|AAL19816.1| (AE008737) ABC superfamily (membrane), putrescine transporter [Salmonella typhimurium LT2]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
/protein_id="AAM86397.1"
/db_xref="GI:21959743"
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QLGLKNVSFAALDSTRFATAEAQIPELVLVNPPRRGIGRELCDYLSQMAPKFILYSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putrescine ABC
/protein_id="AAM86398.1"
/db_xref="GI:21959744"
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fisbslorwdtgliffasivlllldmmcgvavchrrnwarwyvlicqliimiyllmas
                                                /function="transport; transport of small molecules; amino acids, amines"
                                                                                                                                                                                              complement(5462.
                                                                                                                                                                                                                                     /gene="potH"
/note="y2848"
                                                                                                                                                                                                                                                                                                                                 complement(5462.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRLRELDRSIEEAAMDLGATPLKVFFVITVPMIAPALISGWLLAFTLSLDDLVIASFV
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GEIFALLGASGGGKSTLLRMLAGFEQPTQGQIVLDGQDLSHVPFVRRPINMMFQSYAL
FPHMTVEQNIAFGLKQDKLESNEIKSRVAEMLTLVHMQEFAKRKPHQLSEGQRQRVAL
RSLAKRPKLLLLDEPMGALDKKLRDRMQLEVLDILERVGATCVMVTHDQEEAMTMAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="potG"
/function="transport; transport of small molecules;
acids, amines"
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FLLFWLPFLIVEKISLAEMVRAVPPYTDLTTWLDGKLDISLIGONYLLLLDDPLYIDA
YLQSLQVAAVSTLCCLLIGYPLAWAIAHSKPSTRNILLLLVILPSWTSFLIRVYAWA
ILQSLQVALTUWTGIIDQPLVILHTWLAVYIGVVYSYLPFWYLPIYALTRIDYSL
VEAALDLGARPFKTFISVIIPLTKGGIVAGSMLVFIPAVGEFVIPELLGGPDSIMIGR
ILWQEFFNNRDWPVASAVATVMLVLLIAPILWFHKHQNKDIGGAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLSVKAEQAAFNVRRNKRREQEDKLPAPTRINFIFTVNE"
complement(7756. .8982)
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HPLKVDSDASVVDGVPVLVALRPEKVMLCDQVPKDGCNFAVGEVVHIAYLGDLSIYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="residues 1 to 375 of 377 are 86.40 pct identical to residues 28 to 402 of 404 from E. coli Kl2 : 80855"
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/protein_id="AAM86399...
/db_xref="GI:21959745"
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/protein_id="AAM86401.1"
/db_xref="GI:21959747"
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transport system"
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/note="y2849"
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/function="unknown"
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/db_xref="GI:21959746"
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                                                                                                                                                                                                                 OK 73019,
                                                                                                                                                                                                                                                                                                                      OK 73019,
10 (bases
Submitted (02-MAR-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA
                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (27-MAY-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                      OK 73019, USA
12 (bases 1 to 36021)
                                                                                                                                       Submitted (01-MAR-2000) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                Submitted (10-JUN-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (26-NOV-1998) Dep. The University Of Oklahoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-OCT-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                   Direct Submission
                                                                                        Roe, B.A
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Direct Submission
Submitted (13-MAY-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
Direct Submission
Submitted (20-JUN-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-MAY-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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208, Norman,

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On Mar 1, 2000 this sequence version replaced gi:4895277.

Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.

AC004461(119f4) 38146 44873 (0) overlaps AC004462(18c3) 1 6728 (29293) AC004462(18c3) 35015 36021 (0) overlaps AC004471(111f11) 1
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Submitted (27-MAY-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/chromosome="29q11.2"
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4, *** SEQUENCING IN PROGRESS
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moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
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NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 26108 bases at least Q40
Consensus quality: 29530 bases at least Q20
Consensus quality: 31890 bases at least Q20
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                    RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ1-65T079 (1-15) x AC130257 (1-51644)
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,M.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,D., Dathorne,S.R., David,R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
                                                                                                                                                                                                                                                                         AC111766
AC111766.2 GI:21736856
                                                                                                                                                                                                                                                                                                    AC111766 72519 bp D
Rattus norvegicus clone CH230-12122,
***, 37 unordered pieces.
                                                                                                                                                                                  Rattus
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                                                                             Norway rat.
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11551 c 11353 g
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/db_xref="taxon:10116"
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30117: contrag of 1472 b
30217: gap of unknown 1
30217: gap of unknown 1
32310: contrag of 2093 b
32410: gap of unknown 1
33826: gap of unknown 1
33926: gap of unknown 1
35868: contrag of 1942 b
35968: gap of unknown 1
35976: gap of unknown 1
41239: contrag of 1963 b
41239: gap of unknown 1
45188: gap of unknown 1
45188: gap of unknown 1
45188: gap of unknown 1
48447: contrag of 3749 b
48347: contrag of 3749 b
48347: contrag of 3749 b
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Homsi,F., Howard,S., Hubber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mavhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Partmus,E., Pu,L.L., Quiles,M., Ren,Y.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubbkan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Thomas,N., Thomas,S.,
Williamson,A., Warren,R., Washington,C., Watlington,S.,
Williamson,A., Wilczyk,R., Wooden,S., Wang,Q.,
Wu,S., Wu,Y., F., Zhou,J., Zorrilla,S., Nelson,D.,
Direct Suhmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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On Jul 12, 2002 this sequence version replaced gi:18701608
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Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 72519)
Worley, K.C.
Direct Submission
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                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently
consists of 37 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                 as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 38289 bases at least Q40 Consensus quality: 41680 bases at least Q30 Consensus quality: 44356 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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1003: contig of 1003 bp in length 1103: gap of unknown length 2183: contig of 1080 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox.C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabis,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone="CH230-12122"
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Banks,T.,
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                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-MAR-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jul 14, 2002 this sequence version replaced gi:19482300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GTKJ
Center clone name: CH230-105P11
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Center code: BCM
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                                            /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                 /clone="CH230-105P11
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48916:
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81938: contig
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AUTHORS
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Worley, K.C.
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SEQ1-65T079 (1-15) x AC115213 (1-81938)
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                                                                                                                 Carron, T. F., Carter, M., Cavasos, S.R., Chacko, J. Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Claveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davial, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gablis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hagris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hennandez, O., Hodgson, A., Jolivet, S., Joudah, S., Karlyson, E., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Mawhiney, E., McLeod, M.P., Maedor, M., Meit, G., Metzker, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Noger, N., Noger, N., Newtson, J., Newtson, J., Okumon, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Dickerson, E., Nwokasn, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Ward-Moore, S., Warren, R., Washington, C., Wattington, S., Warren, R., Washington, C., Wattington, S., Warren, R., Washington, C., Wattington, S., Walliamson, A., Transy, N., Wolse, R., Williamson, A., Transy, N., Wolse, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wattington, S., Walliamson, A., Transy, N., Shoshington, C., Wattington, S., Walliamson, A., Transy, N., Shoshington, C., Wattington, S., Walley, K., Wang, 
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Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.
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                                                                          Direct Submission
                                                                                                          Weinstock, G. and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 83292)
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Center clone name: CH230-328D17
Center clone name: CH230-328D17
Center clone name: CH230-328D17
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of rea Assembly program: Phrap; version 0.990329
Consensus quality: 55608 bases at least Q40
Consensus quality: 61281 bases at least Q30
Consensus quality: 64903 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonnin,D.,
Bryant, N.P.,
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                                       Allen,C.,
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David, R.,

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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Wa,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Mansey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Moser,M., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Parton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Rulz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
Williamson,A., Warren,R., Washington,C., Watlington,S.,
Williamson,A., Wilczyk,R., Mooden,S., Warley,K.,
Wu,Y., Wu,Y., F., Zhou,J., Zorrilla,S., Nelson,D.,
Ningt Stok,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Depai of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Jul 19, 2002 this sequence version rooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 85022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunarathe,P., Hale,S., Hamilton,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 85022)
                                                                                                                                                        Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 44173 bases at least Q40 Consensus quality: 47255 bases at least Q30 Consensus quality: 49138 bases at least Q20
                                                                                                                                                                                                                                                           Center project Information
Center project name: GYYT
Center clone name: CH230-155L16
                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                 Center: Baylor College
Center code: BCM
Web site: http://www.hg
    soon as it is available preserved.
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                  and the accession number will
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrocks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barboroks, S.L., Amaratunge, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Biange, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davida, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deltaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deltaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deltaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deltaney, K.R., Escotto, M., Fantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, L.E., Johnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC105557
AC105557.2 GI:21736422
HTG; HTGS_PHASE1.
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Rattus norvegicus clone CH230-223K22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 93766)
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/db_xref="taxon:10116"
/clone="CH230-155L16"
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J: GRAD OF CASTA
J: GRAD OF CASTA
J7: CONTIG OF 2518 LF
J7: CONTIG OF 2571 LF
J7: GRAD OF UNKNOWN LENGT
J428: CONTIG OF 316 DF
J4724: CONTIG OF 3196 DF
J4824: GRAD OF UNKNOWN J
J4825: CONTIG OF 3531
J4825: GRAD OF UNKNOWN
JABES GRA
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81466: contig of 3011
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85022: contig of 3456
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22, *** SEQUENCING
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G IN PROGRESS
                  Lewis, L.
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwudnu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rulz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watliamson, A., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Molecular and Human Genetics, Baylor College of Medicine
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18092779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 93766)
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Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990339 Consensus quality: 55649 bases at least Q40 Consensus quality: 59489 bases at least Q30 Consensus quality: 62770 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: GNEM Center clone name: CH230-223K22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------Project Information
                                                                                                                                                                                                                                                                                                                            Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:
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REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL REFERENCE AUTHORS

TITLE

JOURNAL TITLE

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
                                                                                    1122
1222
2308
2408
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3514
              6097
6197
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4814:
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MuznyD. M., Adino-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunky, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, D., Dederich, D.A., Delaney, K.R., Delqado, O., Denn, A.L., Ding, Y. Dinh, H.H., Delaney, K.R., Delqado, O., Denn, A.L., Ding, Y. Dinh, H.H., Delaney, K.R., Delqado, O., Denn, A.L., Ding, Y. Dinh, H.H., Delaney, K.R., Carroll, J., Botto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Harrins, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., King, L., Li, J., 
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Direct Submission

Submitted (19-FEB-2002) Human Genome Sequencing Center, Department Submitted (19-FEB-2002) Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Tarrior Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 12, 2002 this sequence version replaced gi:18701377.
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                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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87797: gap of unknown length
93189: contig of 5392 bp in length
93289: gap of unknown length
9537: contig of 6248 bp in length.
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Direct Submission
Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williamson,A., Wilezyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.P., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S. Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
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Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: Estimated insert size may differ from sequence length
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NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 52457 bases at least Q40
Consensus quality: 55266 bases at least Q30
Consensus quality: 57254 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
------Project Information
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  Tamerisa, A., Tamerisa, K., Tang, H.,
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Bryant, N.P., Bonnin, D., Banks, T., DNA linear HTG 13-JUL-2002
, *** SEQUENCING IN PROGRESS ***,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases_1 to 105756)
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NOTE: This is a 'working draft' sequence. It currently consists of 53 contlys. The true order of the pieces is not known and their order in this sequence record is
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ylor Plaza, Houston, TX 77030, USA
Jul 12, 2002 this sequence version replaced gi:18846366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 54794 bases at least Q40 Consensus quality: 58130 bases at least Q30 Consensus quality: 61124 bases at least Q20
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                                                                                                                                RS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Banbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Brieva, M., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Brown, M., Bryant, N.P., Buck, J., Bowle, S., Cheve, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chowdhry, I., Chistopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Davis, C., Coyle, M., Ford, J., Farraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garzer, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garzer, P., Frantz, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hernandez, J., Howard, S., Huber, J., Hlyk, S., Hume, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, J.C., Lewis, J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lucier, A., Lucier, R., Luna, R., Martindale, A., Martindale, A.
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Rattus norvegicus clone CH230-5G10, *** SEQUENCING IN PROGRESS ***,
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Usmāni,K., Vasquez,L., Vera,V., Vang,S., Ward-Moore,S., Warren,R.,
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97453: contig of 2566 b
97553: gap of unknown 1
101094: contig of 3541 b
101194: gap of unknown 1
105756: contig of 4562 b
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SOURCE

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Query

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Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced g1:15624514.
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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NOTE: This is a 'vorking draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 86463 bases at least Q40 consensus quality; 9329 bases at least Q30 consensus quality; 93219 bases at least Q20 Estimated insert size: 70561; sum-of-contlys estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 0x in Q20 bases; agarose-fp estimation
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation
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40817 40917 42985 43085 44227 44227 44327 45731 45831 47586 49637 49737

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of 1729 unknown of 1951 unknown of 1755 unknown unknown of 1142

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54698 54598:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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VERSION
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LOCUS
DEFINITION
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HUMDGCRCEN
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                                                                                                                                                           61485
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96372815
8776594
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                    Gong, W., Emanuel, B.S., Collins, J., Kim, D.H., Wang, Z., Zhang, G., Roe, B. and Budarf M.L.
A transcription map of the DiGeorge and velo-cardio-faminimal critical region on 22q11
Hum. Mol. Genet. 5 (6), 789-800 (1996)
                                                                                               Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens DiGeorge L77570
                                                  HTG; HTGS_PHASE1.
                                                            AC128996.2 GI:22038427
                                                                          AC128996
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(bases 1 to 108400)
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100717
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                                                                                            norvegicus clone CH230-11M17,
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1. .108400
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89422 90440 90540 90520 92220 92320 93429 93529 94591 94691 94691

90439: 90539: 92219: 92319:

gap of contig gap of contig

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93428: 93528: 94590: 94690: 96150: 96250:

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of 1460 unknown

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84872 84972 86514 86614 88647 88047 88147

86513: 86613: 84971 84871 83670: 83770:

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gap of contig

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74886 74986 76545 76645 77868 77968 77988 79385 79485 80931 81031 81031 81031 81031 81031 81031 81031

74985:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 1, 2002 this sequence version replaced gi:21953916.
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 50052 bases at least Q30
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is
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Submitted (07-FBB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 109396)
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NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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be preserved.
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Center clone name: CH230-15701
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 68820 bases at least Q40
Consensus quality: 73510 bases at least Q30
Consensus quality: 77739 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
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Best Local Similarity:
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Bouck, J. Bowle, S. Brieva, M. Brown, E. Bryant, N. P. Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavacos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cheveland, C.D., Cox, C., Coyle, M.D., Datborne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Fsoster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
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Bryant, N.P.,
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pacca, A., Payton, B., Peetry, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wulliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., E., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        runs of N, but the This record will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.ugsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990339
Consensus quality: 78414 bases at least Q40
Consensus quality: 82108 bases at least Q30
Consensus quality: 85781 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid;
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Chen, G., Chen, R., Chewachry, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Eagn, N., Edward, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gill, R., Earlha, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gill, R., Gabisi, A., Gao, J., Garria, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garria, A., Garner, T., Hale, S., Hamilton, K., Harris, K., Hartis, K., Harti, M., Haylak, P., Hawes, A., Hernandez, J., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jollyk, S., Hume, J., Joudah, S., Kratovic, Kureshi, A., Landry, N., Lead, B., Lewis, L.C., Lewis, L.C., Kureshi, A., Landry, N., Leuter, R., Liu, W., Loulseged, H., Li, J., Li, M., Lau, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Massey, E., Martin, R., Martin, R.,
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barsbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
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99320: gap of unknown 1
104222: contig of 4902 b
104322: gap of unknown 1
109517: contig of 5195 b
109617: gap of unknown 1
114789: contig of 5172 b
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Submitted (24-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherr, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H. Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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NOTE: This is a 'working draft' sequence. It currently consists of 67 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20387295
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Direct Submission
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Center project name: GUYS
Center clone name: CHYS
Center clone name: CHYS
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 94090 bases at least Q40
Consensus quality: 95811 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
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Chavez,D., David, R.,

Bonnin, D., Bryant, N.P., ., Allen,C., Banks,T.,

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                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                        Submitted (18-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., A Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Ba Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonn Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Brya Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C. Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez
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            Center project name: GVVF
Center clone name: CH230-402E14
----- Summary Statistics
                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------Project Information
                                                                                                                                                       Center code: BCM
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Center, Department of Medicine, One

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
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NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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Consensus quality: 92112 bases at least Q40
Consensus quality: 95963 bases at least Q30
Consensus quality: 98562 bases at least Q20
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Muzny, D.M., Adams, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Auzny, D.M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Bimage, K., Brown, E., Brown, M., Bryant, N.P.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Baylor Plaza,
On Aug 24, 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 122517)
Worley.K.C.
Direct Submission
Submitted (18-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 122517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, K., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Ward-Moore, S., Warren, R., Washington, C., Watliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-AUG-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
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Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid;
Sequencing vector: M13;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 58% of reads
Chemistry: Dye-terminator Big Dye: 42% of read
Assembly program: Phrap; version 0.990329
Consensus quality: 70875 bases at least Q40
Consensus quality: 76728 bases at least Q30
Consensus quality: 79150 bases at least Q20
                                                                                                                                                        as soon as it
be preserved.
                                                                                                                                                                             (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                             Aug 24, 2002 this sequence version replaced gi:21953961.
                                                                                                                                                                                                                                                                                                                                                                       Center project name: TUEA
Center clone name: CH230-1B16
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Center code: BC
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    Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,

Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,

Buhay, C., Burch, P., Burkett, C., Burrell, K. L., Byrd, N. C.,

Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,

Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,

Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,

Falls, T., Ferraguto, D., Flagg, N., Ford, J., Escotto, M., Frantz, P.,

Gabisi, A., Gao, J., Garcia, A., Ganner, T., Garza, N., Gill, R.,

Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K.,

Harris, C., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,

Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.

Li, J., Li, X., Lucier, A., Martindele, A., Martinez, E.,

Maheshwari, M., Mapua, P., Martin, R., Martinez, E.,

Mansey, E., Mawhiney, E., McLeod, M. P., Meador, M., Morris, S.,

More, N., Martinez, E., McLeod, M. P., Meador, M., Morris, S.,

More, N., Martinez, E., McLeod, M. P., Meador, M., Morris, S.,

More, N., Martinez, E., McLeod, M. P., Meador, M., Morris, S.,

More, N., Martinez, E., McLeod, M. P., Meador, M., Morris, S.,

Martinez, E., McLeod, M. P., Meador, M., Morris, S.,

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Nguyen, A., Nguyen, N.,
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Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pacce, A., Payton, B., Peerry, J., Percez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubkan, I., Rolie, M., Rulz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watliamson, A., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-JUL-2002) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicin Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced g1:17974587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 124579)
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NOTE: This is a 'vorking draft' sequence. It currently consists of 84 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 23868 bases at least Q40
Consensus quality: 26331 bases at least Q30
Consensus quality: 28175 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
-------- project Information
Center project name: GJFC
Center clone name: CH230-47P11
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    Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferragutto, D., Flagg, M., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gabriel, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Garris, C., Hartis, K., Hatt, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Karatovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Mardor, M., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Orragunye, N., Ovtedo, R., Pace, A., Patton, B., Pacer, J.,
Orragunye, N., Ovtedo, R., Pace, A., Patton, B., Pacer, J.,
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                                                                                                                                                                                                                                                                                                                                                       Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., 1
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Allen,C.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Molecular and Human Genome Sequencing Center, Department Baylor Plaza, Houston, TX 77030, USA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 41 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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be
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Contact: hgsc-help@bcm.tmc.edu
----- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-562E17 is from the library RPCI-11.2 constructed by the group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sections only once, except for a short overlap. The true right end of clone RP11-562E17 is at 1 sequence. The true right end of clone RP11-217F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Sep 14, 2001 this sequence version replaced gi:15131959. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone RP11-562E17 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP11-562E17 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human DNA sequence from clone RP11-562E17 on chromosome 13,
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                                                                                                                                                                                                                                       /clone_lib="RPCI-11.2"
23798 c 24651 g 45
                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /clone="RP11-562E17"
                                                                                                                                                                                                                                                                                                                                               /chromosome="13"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                    Falls, T., Ferraguto, D., Fladgy, M., Ford, J., Foscer, P., Falts, T., Ferraguto, D., Fladgy, M., Ford, J., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jair, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratcvic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mahsshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeedd, M.P., Meador, M., Mei, G., Metzker, M., Moser, M., Nickerson, E., Nwchenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pitkerson, E., Nwchenkwo, S., Oguh, M., Okwuonu, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonakke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, N., Thomas, N., Thomas, N., Thomas, N., Walllams, G., Walltanson, A., Waleczyk, R., Wooden, S., Watlingson, S., Walltanson, S., Walczyk, R., Wooden, S., Watlington, S., Weinstock, G. and Gibbs, R.
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                          Submitted (27-JAN-2002) Human Genome Sequencing Center, Departed Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Edwards, C.C., Elhaj, C., Escotto, M., Edwards, C.C., Elhaj, C., Escotto, M., Escotto,
                                                                                                                                                      Direct Submission
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Rattus norvegicus clone CH230-303C16,
***, 65 unordered pieces.
AC108328
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                                                                                                                                                                                                                                                              Unpublished
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ylor Plaza, Houston, (bases 1 to 147108)
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Burkett,C., Burrell,K.L., Byrd,N.C
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                                                                                                           nepartment
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	COMMENT	AUTHORS TITLE JOURNAL
	Daylor plaza, Houston, TX 77() On Jul 12, 2002 this sequence	Worley, K.C. Direct Submission Submitted (13-JUL-2
	man Genetics, Baylor College on, TX 77030, USA sequence version replaced (College of Medicine	002) Human Genome Sequencing Center, Depar
Alignment Scores Pred. No.: Score: Score: Percent Similari Best Local Simil Query Match:	**********************	* * * *
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Baylor Plaza, Houston,
3 (bases 1 to 148879)
                                                                                                   Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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*** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently
consists of 59 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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RESULT 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-513115 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-513115 is at 1 in this sequence. The true left end of clone RP11-187N21 is at 149829 in this sequence. The true right end of clone RP13-459B11 is at 22924 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on Jul 25, 2001 this sequence version replaced g1:14626095. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
AL354740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP11-513I15 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 6, constructed by the Sanger Centre Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP11-513115 is from the library RPCI-11.2 const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; SINISPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 151828)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            database can be found at
                              /note="19 co
2402. .2438
/note="MIR r
2741. .2833
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                                                                                                                                                                                                        /clone_lib="RPCI-11.2"
1538. .1622
                                                                                                                                                    2003. .2078
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                   /clone="RP11-513115"
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="MIR repeat: matches 49.
                                                                                                                                                                             /note="MIR repeat: matches 82. .165 of consensus"
                                                                                                                                                                                                                                                                                                     /chromosome="6"
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                                                                                                                  19 copies 4 mer cctc 71%
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   .145 of consensus'
                                                          .131 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                        /note="13 copies 4 mer tgga 73% conserved" 21930. .21969
                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
22774. .22866
                                                                                                                                                                                                                                                                                                                                                  /note="CpG island"
                                                                            /note="AluJb repeat:
                                                                                                                             /note="L1ME3 repeat: matches 5833. .6088 of consensus"
24392. .24697
                                                                                                                                                                                                           /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                         note="MER5B repeat: matches 101. .171 of consensus"
                                                                                                                                                                                                                                                                         /note="FLAM_C repeat: matches 1.
                                                                                                                                                                                                                                                                                                       /note="MER5B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15240. 15279

Moote="5 copies 8 mer tgaatgaa 92% conserved"

15688. 15795

Moote="9 copies 12 mer 79% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 34. .169 of consensus"
14915. .15111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="4 copies 12 mer 89% conserved"
12903. 12950
note="6 copies 8 mer gagcgagc 81% conserved"
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/note="AluJb repeat: matches 1.
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note="MER46C repeat: matches 12. .338 of consensus"
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te="MIR repeat: matches 108.
43. .21281
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60. .13621
                                                                                                                                                                                                                                                                                                                                                                                       e="5 copies 8 mer acacacac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 6864
:e="L2 repeat: matches 2438.
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.12948
                                                                                                                                                                7 copies 4 mer gaaa 92% conserved"
.24357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    copies 65 mer
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                                                                                                                                                                  /note="23 copies 38619. .39430
                                                                                                                                                                                                                                                                                                                                                                            /note="AluSx repeat: matches 1. 37221. .37795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30114. .30291

/note="AluSx repeat: matches 151. .312 of consensus"

30292. .30593

/note="AluSy repeat: matches 1. .302 of consensus"

30594. .30739
                                                                                                                                                                                                                                     /note="25 copies 2 mer aa 72% conserved" 38190. 38503 /note="Aluxx repeat: matches 1. .312 of 38504. .38613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJo repeat: matches 3. .296 of consensus"
27586. .27736
/note="LIMC4 repeat: matches 7237. .7390 of consensus"
27737. .28033
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Alusx repeat: matches 134.
36788. .37076
note="Alusx repeat: matches 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28638. .28816
/note="AluSg/x repeat: matches 131. .312
29512. .29659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSg/x repeat: matches 121. .132 of consensus"
28345. .28637
                                                                                                                                                                                                                                                                                                                          note="4 copies 12 mer 87% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 3.
36621. .36787
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/note="AluSp repeat: matches 1.
35275. .35552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="L1MA2 repeat: matches 3482. .6110 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 3.
32235. .34816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1MA2 repeat: matches 2720. .3482 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MSTA repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1MA2 repeat: matches 6110. .6308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluSg repeat: matches 3. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L2 repeat: matches 1995. .2150 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 7389. .7440
                                             Length:
Matches:
Conservative:
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                                                                                                                                                                                                                           Submitted (27-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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21, *** SEQUENCING IN PROGRESS
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as i
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Chemistry: Dye-terminator Big Dye: 100% of Assembly program: Phrap; version 0.990329
Consensus quality: 124262 bases at least (Consensus quality: 128161 bases at least (Consensus quality: 131092 bases at least (C
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Project Information
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AL Submitted (01-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CBH0 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 23, 2000 this sequence version replaced gi:9368089.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
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Em: EMBL; Sw:, SWISSPROF; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                        Direct Submission
Submitted (12-JUN-1998)
University School of Med
                                                                                                                                                                                                      2 (bases 1 to 154616)
Ryan, E., Sun, H. and Spalding, L.
The sequence of Homo sapiens PAC clone RP4-647C14
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                 Waterston, R.H.
Direct Submission
                                                                                                                                       Waterston, R.H.
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restrition enzyme digest data."
a 31281 c 29218 g 47730 t
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/chromosome="1"
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1. .154588
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                                                                                            98) Genome
Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154616 bp DNA linear PRI 08-NOV-200
PRP4-647C14 from 14q24.3, complete sequence.
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Matches:
                                                                                        Sequencing Center, Washington 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence are more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE INFORMATION:
This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the compact of the compac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone from chromosome 14 was provided by Roswell Park Cancer Institute, Human Genetics Carlton Streets, Buffalo NY 14263-0001 USA.
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University, 4444 Forest
6 (bases 1 to 154616)
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5 (bases 1 to 154616)
                                                                                                                                                                                                                                                                                                                          The sequence from position 141555 product of RP4-647C14 PAC DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                The sequence RP4-647C14 contains a dinucleotide AT position 4427 to 4478. The exact number of copies determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the left is RP1-240K6; the clone sequenced to the right is RP4-687K1. Actual start of this clone is at base position 197 of RP4-647C14; actual end is at base position 730 of RP4-687K1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one male donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_DJ0647C14
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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   /rpt_family="Alu" 288. .319
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                                                                                                                                                                              /db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                     clone="RP4-647C14"
clone_lib="RPCI-4"
                                                                                                                                                     /map="14q24.3"
                                                                                                                                                                                                                                        organism="Homo sapiens"
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Park Avenue, St. Louis,
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Missouri 63108,
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artment, Elm and
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/note="similar t
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7363. .7649
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4807. .5214
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3955. .4079
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2993. .3023
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7051. .7357
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Search completed: January 28, 2003, 12:15:22  
Job time: 1666.67 secs
                                               Db
                                                                     QΥ
                                                                                          SEQ1-65T079 (1-15) x AC004846 (1-154616)
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                                                                                                                                                                              Alignment Scores: Pred. No.:
                                            misc_feature
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10459. .10757
/rpt_family="Alu"
10899. .11021
                                                                                                                                                                                                                                                                                                                                  /rpt_family="MER2_type"
9092. .9459
/rpt_family="L2"
9496. .9671
                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu"
8221 ..8560
/rpt_family="MER1_type"
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Matches:
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Command line parameters:

MODEL-frame+_p2n.model -DEV-xlh
-MODEL-frame+_p2n.model -DEV-xlh
-Q-/Ggn2_1/USPTO_SPOOL/SORING82/runat_23012003_130140_7866/app_query.fasta_1.597
-DB-N_Geneseq_101002 -QFMT-fastap -SUFFIX-01ip2n.rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MAXTRIX-01ig0 -TRANS-human40.cdi
-LIST-1000 -DOCALIGN-200 -THR_SCORE-quality -THR_MIN-8 -ALIGN-50 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-BORIN682_@CGN_1_1187_@runat_23012003_130140_7866 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NE_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN TIMEOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -FGAPOXT-7
-YGAPOP-60 -YGAPEXT-60 -DELEXT-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 1000 summaries
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Ygapop 60.0
Fgapop 6.0
Delop 6.0
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           N_Geneseq_101002:*
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| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.bAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA198.DAT:*
| SIDS2/gcgdata/geneseq/geneseqn-emb1/NA199.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000, DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being priand is derived by analysis of the total score distribution. being printed,

Hone D, Shata M,

Lewis G, I Agwale S;

Fouts 'n

Bagley K,

Boyson M,

Obriecht

ü

(UYMA-)

UNIV MARYLAND BIOTECHNOLOGY INST.

WPI; 2002-383031/41.

Co-expression DNA vaccines comprising an antigen-encoding region and a

SUMMARIES

28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	c 12	11	10	9	8	7	σ	5	4	ω	N	1	Result No.
8	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	12	15	15	15	15	15	15	15	15	15	15	15	Score
53.3	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	80.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
40	711	711	711	711	711	711	711	711	711	711	711	711	711	711	711	40	1514	1508	1152	1148	1143	782	782	782	777	777	723	Length
21	20	14	14	14	14	14	14	14	14	14	14	14	14	14	14		22			13	24	21	21	21	6	6	24	DB
AAA51114	AAV81595	AAQ42768	AAQ51326	AAQ51325	AAQ51324	AAQ51323	AAQ51322	AAQ51321	AAQ51320	AAQ51319	AAQ51318	AAQ51317	AAQ51316	AAQ51315	AAQ51314	AAA51140	AAS01505	AAS01506	ABL40639	AAQ23864	ABL40640	AAA51544	AAA51147	AAA51106	AAN50206	AAN50205	ABK50864	ID
Oligomer sLT-A For	ŗ	E.coli heat labile	Encodes Lys-114 E.		Encodes Ser-106 E.	Encodes Ser-104 E.	-104	04	Encodes Glu-107 E.	Encodes Tyr-97 E.c	Encodes Lys-97 E.c	Encodes Lys-63 E.c	Encodes Tyr-53 E.c	53	Asp-53	Oligomer sLT-A Rev	۳.	E. coli heat-labil	E. coli heat-labil	Thermolabile toxin	ᠴ			ptimized	Sequence of the pi	Sequence of the pi	Escherichia coli h	Description

ALIGNMENTS

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RESULT 1
ABK50864
ID ABK5
08-SEP-2000; 2000US-231070P.
08-SEP-2000; 2000US-231376P.
08-SEP-2000; 2000US-231403P.
08-SEP-2000; 2000US-231449P.
                                                                                                                                                                                                                                                                                                                                                                   Co-expression DNA vaccine; antibacterial; antiviral; antiparasitic; immunostimulant; vaccine; immune response; systemic tolerance; Tat-mediated immune deviation; ds; heat labile enterotoxin sub-unit
                                                                                                                                                                                                 14-MAR-2002.
                                                                                                                                                                                                                                                         WO200219968-A2.
                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli heat labile enterotoxin sub-unit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK50864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK50864 standard; DNA; 723 BP.
                                                                                                                                         10-SEP-2001; 2001WO-US28365
                                                                                                                                                                                                                                                                                                                                                                      sub-unit A.
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Best Local Si
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                             E.coli NCIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inducing significantly stronger immune responses against vaccine antigens than conventional DNA vaccines, and are also capable of inducing systemic tolerance. This sequence represents the Eschericali heat labile enterotoxin sub-unit A that up-regulates CAMP LE The enterotoxin is an immunoregulatory molecule useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 active component such as adjuvants, immunoregulatory peptides and proteins, antisense RNAs, and catalytic RNAs. The co-expression DNA vaccines are useful for vaccinating animals against viral, bacterial and parasitic pathogens, for enhancing immune responses, for inducir systemic tolerance, and for treating and/or preventing Tat-mediated immune deviation. The co-expression DNA vaccines are capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a new DNA vaccine comprising a region encoding an antigen component and a region encoding at least one biologically
                                                 WPI; 1985-148358/25
P-PSDB; AAP50190.
                                                                                                                                                                  12-DEC-1984;
                                                                                                                                                                                          19-JUN-1985
                                                                                                                                                                                                                   EP145486-A
                                                                                                                                                                                                                                                                                                                    Pig scours vaccine;
                                                                                                                                                                                                                                                                                                                                             Sequence of the pig
                                                                                                                                                                                                                                                                                                                                                                                               AAN50205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 723 BP; 238 A; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 12; Page 89; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biologically active component-encoding region, useful as vaccines against viral, bacterial and parasitic pathogens, or for enhancing
                        New toxoid as inactivated form of toxin for
                                                                                                               (GLAX ) GLAXO GROUP LTD
                                                                                                                                         12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                       AAN50205 standard;
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           from organism transformed by gene
                                                                                         Harford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA vaccines described in the invention.
                                                                                                                                         83GB-0033131
                                                                                                                                                                 84EP-0308620
                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             scours
                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                       777
                                                                                                                                                                                                                                                                                                                                           heat labile toxin (LT) LTA gene
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                                                                                       GW
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CAMP levels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN50205 is the gene sequence of the natural LTA gene. The LTA ge the site directed mutant SDM1 (see AAN50206) is inactive. The inventors claim a vaccine prepr. active against pig scours which contains an inactivated LTA component, together with additional K antigens opt. with whole cells component the antigens opt.
      AANSO205 is the gene sequence of the natural LTA gene. The LTA getthe site directed mutant SDMI (see AANSO206) is inactive. The inventors claim a vaccine prepn. active against pig scours which contains an inactivated LTA component, together with additional realizers opt. with whole cells comprising the antigens or contg.
                                                                                           New toxoid as inactivated obtd. from organism trans
                                                                                                                                          WPI; 1985-148358/25
                                                                                                                                                              Hayes MV,
                                                                                                                                                                                                                                                    19-JUN-1985
                                                                                                                                                                                                                                                                         EP145486-A.
                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                         E.coli NCIB
                                                                                                                                                                                                                                                                                                                                                                                            Pig scours vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of the pig scours site directed mutant SDM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN50206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigens opt. with whole cells comprising the antigens or contg. the inactivated LTA.
                                                                        Example; Fig 2; 61pp; English
                                                                                                                               P-PSDB;
                                                                                                                                                                                   (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                        12-DEC-1983;
                                                                                                                                                                                                                              12-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAN50206 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly
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235..237
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                                                                                                        form of toxin
                                                                                                                                                                                                                                                                                                                                                                                             diarrhoea;
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                                                                                                        for use
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                                                                                                        in vaccines
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
This plant-codon optimized cDNA encodes a synthetic Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accompdate the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the
                                                                                             New polynucleotides encoding LT-A transformation of plant cells, use elicit immune responses in animals
                                                                                                                                                                         (BOYC-)
(MASO/)
(ARNT/)
                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                    Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                             Plant-optimized E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA51106 standard; cDNA; 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2000
                                                                             Example 1; Fig 1; 103pp; English.
                                                                                                                                                                                                                              22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                             22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 AGTTTGAGAAGTGCTCACTTAGCAGGACAGTCTATATTATCAGGA
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                                                                                                                                         2000-442653/38.
                                                                                                                                                        HS, Arntzen CJ,
                                                                                                                                                                         BOYCE THOMPSON INST PLANT MASON H S. ARNTZEN C J.
                                                                                                                                AAY96646.
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                                                                                                                                                                                                                                                                                                                                                                   coli.
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57..779
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                     CT-A polypeptides for the in immunogenic composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223
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RESULT 5
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (CT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the production of treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adjuvant; anti-bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 782
                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant-optimized E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA51147;
elicit
           New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositi
                                                             P-PSDB;
                                                                                                                                                                                                       22-DEC-1998;
                                                                                                                                                                                                                                      22-DEC-1999;
                                                                                                                                                                                                                                                                      29-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No . :
                                                                                                                                          (ARNT/)
                                                                                                                                                       (BOYC-) BOYCE THOMPSON INST PLANT RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly
                                                                             2000-442653/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTTGAGGTCTGCTCACTTGGCAGGACAATCCATCCTCTCAGGA
                                                                                                            , SH
immune responses in animals
                                                              AAY96647
                                                                                                            Arntzen CJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli.
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/*tag= b
60..779
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3..782
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Matches:
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103pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants. Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A cDNA shown in AAA51106 which is given in Figure 1 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NcoI restriction site around the initiator methionine codon. Novel polynucleoties encode a mutant LT-A polypeptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one compared to the wild-type LT-A or CT-A polypeptide and where at least one
(MASO/) MASON
                                                                       22-DEC-1999;
                                                                                                        29-JUN-2000
                                                                                                                                    WO200037609-A2
                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                             adjuvant; anti-bacterial; R192G; ss.
                                                                                                                                                                                                                                                                                                                                                                                         Plant-optimized E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant-preferred codons and eliminates sequence motifs associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA encodes a mutant S63K Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The codon at nucleotide positions 246-248 was changed from the wild-type TCC to AAG which causes a change of serine to lysine in the mature protein at residue 63. The sequence contains
                                          22-DEC-1998;
                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                               Heat-labile toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA51544 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
THOMPSON INST PLANT RES
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3..59
                                           98US-0113507
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                                                                                                                                                               /*tag=
60..779
/*tag=
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15.00
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21
                                                                                                                                                                                                                                                                                                                                                          LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
                                                                                                                                                                                                                                                                                                                                                                                      coli LT-A G192 mutant coding sequence
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                             ABL40640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mature protein at residue 192. The sequence contains plant-preferred CC codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NcoI restriction site around the codon intiator methionine codon. Novel polynucleotides encode a mutant LT-A colory peptide or a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further CC comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the production of the mutant polypeptides are also useful as adjuvants.

Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A cDNA shown in AAA51106 which is constructed from the wild type LT-A cDNA shown in AAA51106 which is
                                   misc_feature
                                                                                                                                       Escherichia
                                                                                                                                                                       vaccine; mutant;
                                                                                                                                                                                       LT; heat-labile toxin; cholera toxin; CT; recombinant; adjuvant.
                                                                                                                                                                                                                       E. coli mutant heat-labile toxin (mLT) 5B-SD-1A protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No . :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A subunit (LT-A). The nucleotide at position 631 was changed from the wild-type A to G which causes a change of arginine to glycine in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals
                                                                                                                                                                                                                                                          17-JUN-2002
                                                                                                                                                                                                                                                                                          ABL40640
                                                                                                                                                                                                                                                                                                                           ABL40640 standard; DNA; 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                              252
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                                                                                                                                                                                                                                                                                                                                                                                                           SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly
                                                                                                                                                                                                                                                                                                                                                                                              AGCTTGAGGTCTGCTCACTTGGCAGGACAATCCATCCTCTCAGGA
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                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                             /note= "contains
1..312
/note=
                 /*tag=
                                                                                    Location/Qualifiers
1..1143
                                                                                                                                                                       mLT;
                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 A; 186 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The nucleotide at position 631 was changed from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a mutant R192G Escherichia coli heat-labile toxin (LT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.00%
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 "mLT 5B subunit'
                                                                                                                                                                                                                                                                                                                           ВP
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a gene encoding a protein having a subunit structure of IA5B in which the DNA sequence encoding each signal is deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene)-(SD sequence gene)-(A subunit gene). A method is provided for the preparation of a protein having a subunit structure of IA5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli mutant heat-labile toxin (mLT) 5B-SD-1A protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DOKU-) DOKURITSU GYOSEI HOJIN NOGO
(HGET ) HIGETA SHOYU KK.
(FUJI-) FUJITA GAKUEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 12-13; 27pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparation of a protein having 1A5B structure
                                     JP04079898-A
                                                                                      LTh; ST1a; ST1b; t probe; detection;
                                                                                                                           Thermolabile toxin (LTh) gene
                                                                                                                                                     08-OCT-1992 (first entry)
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                                                              Esherischia coli.
                                                                                                                                                                                                            AAQ23864 standard; DNA; 1148 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1143 BP;
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                                                                                                 thermolabile; heat-stable; E.coli; T4DNA ligase;
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Gaps:
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07-AUG-2000; 2000JP-0238740

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13-MAR-1992.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-2002
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                                                                                                                                                                                             /*tag= c
/note= "SD sequence"
340..1152
                                                                                                                                                                                                                                                                                                           /note= "LT 5B
313..339
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                                                                                                                                                     "LT
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a gene encoding a protein having a subunit structure of 1A5B in which the DNA sequence encoding each signal is deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene) - (SD sequence gene) - (A subunit gene). A method is provided for the preparation of a protein having a subunit structure of 1A5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coll heat-labile toxin (LT) 5B-SD-1A protein encoding DNA.
   15-SEP-1999;
                                                          15-SEP-1999;
                                                                                                                                                                               WO200119998-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli heat-labile enterotoxin (LT) mutant LTdel110/112 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS01506;
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)B; ABB07784.
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HIGETA SHOYU KK.
FUJITA GAKUEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli strain K88ac.
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                                                          99WO-KR00555
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/transl_except= (pos:932..933,aa:Met)
/note= "This codon has an apparent 1 nu
deletion which alters the readin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Groups of mice were immunised with ITS623Y or LTdell10/112. The control groups received phosphate buffered saline (PBS) alone. The serum and faecal antibody titres to LT were determined. The results showed that mice immunised with LTS63Y or LTdell10/112 contained high and comparable level of anti-LT antibodies in sera and faecal extracts compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are two novel detoxified and immunologically active proteins (LT mutants) derived by site-directed mutagenesis of the Al subunit of wild type LT. The substitution of Ser to Tyr at position 63 in LT8637 blocks NAD-binding. Deletion of Glu residues at positions 110 and 112 in LTde1110/112 eliminate the enzymatic activity of LT. The Al subunit of wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein the regulates CAMP levels. The resulting increase in CAMP is the cause of diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities of mutant heat-labile endotoxins LT8637 and LTde1110/112 were tested.
                                                                                                               Escherichia Synthetic.
                                                                                                                                                         Heanchabahe enhero toxin; LT; LTS63Y; LTdell110/112; mutant; detoxified and immunologically active protein; ADP-ribosylation; Gs; endotoxin; diarrhoea; ds.
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                                                                                                                                                                                                                                                                                                      AAS01505;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 45-46; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful as vaccine for preventing for antibody production -
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                                                                                                                                                                                                                                coli heat-labile enterotoxin (LT) mutant LTS63Y
                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                coli strain K88ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence encodes for Escherichia coli heat-labile
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/tag= a
/product= "LTS63Y mutant protein"
/transl_except= (pos:938..939.aa.Met)
/note= "This codon has an apparent 1:
                                                                 164..1311
                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches: Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coli heat-labile enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AAU00506) and LTdell10/112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diarrhoea, and as adjuvant
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15
0
0
                                                                                                                                                                                                                                  DNA
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New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as adjuvant for antibody production -
                                                                                                                                                                                                                                            15-SEP-1999;
                                                                                                                                                                                                                                                        15-SEP-1999;
                                                                                                                                                                                                                                                                       22-MAR-2001
                                                                                                                                                                                                                                                                                    WO200119998-A1
                                                                                                                                                   Claim 3; Page 41-42; 48pp; English
                                                                                                                                                                                                                 Park EJ,
                                                                                                                                                                                                                             (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
                                                                                                                                                                                                   2001-281524/29
                                                                                                                                                                                                                Kim JS, Chang J,
                                                                                                                                                                                                                                           99WO-KR00555
                                                                                                                                                                                                                                                        99WO-KR00555
                                                                                                                                                                                                                                                                                                 deletion which alters the reading frame"
                                                                                                                                                                                                                Yum J,
                                                                                                                                                                                                                Chung
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The present sequence encodes for Escherichia coli heat-labile centerotoxin (LT) mutant LTS63Y and LTG61110/112 (AAU00507) CC are two novel detoxified and immunologically active proteins (LT mutants) derived by site-directed mutagenesis of the A1 subunit of wild type LT. The substitution of Ser to Tyr at positions 110 and 112 in CC (Togel110/112 eliminate the enzymatic activity of LT. The A1 subunit of CC (Togel110/112 eliminate the enzymatic activity of LT. The A1 subunit of CC (Togel110/112 eliminate the enzymatic activity of LT. The A1 subunit of CC (Togel110/112 eliminate of CC (Togel110/112 elim for antibody production. that

Alignment Scores: Pred. No.: 1514 0 0 0

Sequence 1514 BP; 510 A; 277

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298

<u>ი</u>;

429 Η.

0 other;

Percent Similarity:
Best Local Similarity:
Query Match: 1.79e-06 15.00 100.00% 100.00% 100.00% 22 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

용 Š 1 SerLeuArgSerAlaHisLeuAlaGlyGlnSerIleLeuSerGly 15 SEQ1-65T079 (1-15) x AAS01505 (1-1514)

RESULT 12 AAA51140/c AAA51140 standard; DNA; 40 ВÞ

Oligomer sLT-A Rev-14 for LT-A cDNA synthesis 26-SEP-2000 (first entry)

Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; adjuvant; anti-bacterial; ss. oral;

Escherichia coli

CC Oligonucleotide 40-mers (AAA51107-26) spanning the entire synthetic CC Escherichia coli heat-labile toxin (LT) A subunit (LT-A) coding sequence CC and a set of complementary 40-mers (AAA51127-46) that centre on the CC junctions of the coding oligomers allowing 20 bp overlaps were obtained CC commercially and used to construct the synthetic LT-A cDNA. The sequence CC contains plant-preferred codons and eliminates sequence motiffs CC encoding valine) was made to accommodate the creation of a Ncol CC encoding valine) was made to accommodate the creation of a Ncol CC entriction site around the initiator methionine codon. Novel CC cholerae cholera toxin (CT) A subunit (CT-A) polypeptide or a mutant Vibrio CC cholerae cholera toxin (CT) A subunit (CT-B) olypeptide, which have CC polypucled and where at least one of the codons is altered to a plant CC polypeptide and where at least one of the codons is altered to a plant CC preferred codon. The polypucleotide further comprises a nucleic acid conjuncted codon. The polypucleotide further comprises a nucleic acid conjuncted or CT B subunit (CT-B). The CC polypucleotides are useful for the transformation of plant cells for the production of transgenic plants for the prophylactic or therapeutic CC creatment against E. coli or V. cholerae. The mutant polypeptides are conserved as adjuvants. (BOYC-) BOYCE THOMPSON INST PLANT RES (MASO/) MASON H S. (ARNT/) ARNTZEN C J. Example 1; Fig 2; 103pp; English. elicit immune responses in animals New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions WPI; 2000-442653/38 22-DEC-1998; Mason HS, Arntzen CJ; 22-DEC-1999; WO200037609-A2 Synthetic 98US-0113507 99WO-US30747

ç

Sequence 40 B₽; 11 A; 9 C; 13 <u>ດ</u> 7 T; 0 other;

Query Match: DB: SEQ1-65T079 (1-15) x AAA51140 (1-40) Percent Similarity: Best Local Similarity: Pred. No.: Alignment Scores: 8.45e-05 12.00 100.00% 100.00% 80.00% 21 Length:
Matches:
Conservative:
Mismatches:
Indels: 0 0 0 0 1 4 0

RESULT 13

Вþ

AAQ51314

AAQ51314 standard; DNA; 711

08-DEC-1993 (first entry)

enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity;

Encodes Asp-53 E.coli heat labile toxin subunit A.

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RESULT 14
AAQ51315
ID AQ51
XX AAQ51
AC AAQ51
XX O8-DE
XX O8-DE
XX O8-DE
XX ORTER
XX 
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DB:
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                                                                       enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A;
protomer A; site-directed mutagenesis; reduced toxicity;
ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                        08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenic, detoxified LT-A proteins and their use in vaccines protect against enterotoxigenic E.coli. Sequence AAQ51314 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al., J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to
                          Escherichia coli
                                                                                                                                                                                Encodes Glu-53 E.coli heat labile
                                                                                                                                                                                                                                                                                                                                       AAQ51315 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                       AAQ51315;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOC-) BIOCINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                         190 AGTTTGAGAAGTGCTCACTTAGCAGGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SerLeuArgSerAlaHisLeuAlaGlyGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1993-227320/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 A;
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10.00
100.00%
100.00%
66.67%
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Mismatches:
Indels:
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RESULT 15
AAQ51316
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                       Key Location/Qualifiers
misc_difference 153..155
                                                                                                enterotoxigenic bacteria; vaccine; imm
protomer A; site-directed mutagenesis;
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P-PSDB;
                                                              Escherichia
                                                                                       ADP-ribosyltransferase
                                                                                                                                      Encodes Tyr-53 E.coli heat labile toxin subunit A.
                                                                                                                                                                08-DEC-1993
                                                                                                                                                                                                                AAQ51316 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic detoxified mutant cholera toxin and heat labile - useful as vaccines against infection by Vibrio cholerae an enterotoxin producing Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 711
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                                                                                                                                                                                                                                                                AGTTTGAGAAGTGCTCACTTAGCAGGACAG
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DB; AAR38731.
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                                                              coli
                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP;
                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 153..155
/note= "wild-type GTC(Val) mutated to TAC(Tyr)"
              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "wild-type GTC(Val) mutated to GAA(Glu)"
                                                                                                                                                                                                                                                                                                                                                                                                                                          236 A; 122 C;
                                                                                                                                                                                                                                                                                                                                      0.14
10.00
100.00%
100.00%
66.67%
                                                                                                                                                                                                                DNA;
                                                                                     activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPA.
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                                                                                                 vaccine; immunogenic detoxified LT-A;
mutagenesis; reduced toxicity;
                                                                                                                                                                                                               ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                        156 G;
                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
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Conservative:
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RESULT 16
AAQ51317
ID AAQ51
XX AQ51
XX O8-DE
DT 08-DE
DT 08-DE
DX Encod
XX enter
KW enter
KW ADP-r
XX Esche
XX O8-JU
PD 08-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment
Pred. No.
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                                                                                                                                                       enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity; ss.

    useful as vaccines against infection
enterotoxin producing Escherichia coli

08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 2 and Page 46; 60pp; English.
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                                                                                                                             Escherichia
                                                                                                                                                                                                                Encodes Lys-63 E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                           08-DEC-1993 (first entry)
                                                                                                                                                                                                                                                                                                   AAQ51317 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic detoxified mutant cholera toxin and heat labile toxin
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                             W09313202-A
                                                                                    misc_difference
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DB; AAR38732.
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                                                                                  Location/Qualifiers 184..186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 A; 123 C; 155 G; 198 T; 0 other;
                                                      /note= "wild-type TCT(Ser) mutated to AAG(Lys)"
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RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenic, detoxified LT-A proteins and their use in vaccines t protect against enterotoxigenic E.coli. Sequence AAQ51317 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                        enterotoxigenic bacteria; vaccine; immunogenic detoxified protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
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Domenighini M,
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P-PSDB; AAR44018.
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                                                                      (BIOC-) BIOCINE SCLAVO
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                                                                                                                                                                                            /note= "wild-type CAC(His) mutated to GAG(Glu)"
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterotoxigenic bacteria; vaccine; immunogenic detoxifie protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
                   Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                           enterotoxin
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The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto
                                                          Immunogenic detoxified mutant cholera toxin and heat labile - useful as vaccines against infection by Vibrio cholerae an enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxigenic bacteria; vaccine; immunogenic detoxified protomer A; site-directed mutagenesis; reduced toxicity;
                                      Claim 3; Fig
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DB; AAR44021.
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The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines t protect against enterotoxigenic E.coli. Sequence AAQ51322 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                   Claim
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protomer A; site-directed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protect against enterotoxigenic E.coli. Sequence AAQ51323 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amir acid numbering is based on the cholera toxin A subunit sequence
          protect against enterotoxigenic E.coli. Sequence AAQ51324 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amir
                                                                       toxin (LT-A) of a strain of
et al, J.Biol. Chem., 259,
site-directed mutagenesis.
                                                                                                                                                              Immunogenic detoxified mutant cholera to useful as vaccines against infection enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterotoxigenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encodes Ser-106 E.coli heat labile toxin subunit A.
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primer sequence used to introduce the pacid numbering is based on the cholera
                                                site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines
                                                                                                               The wild-type
                                                                                                                                         Claim
                                                                                                                                                                                                                                                     Domenighini M,
                                                                                                                                                                                                                                                                              (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                       31-DEC-1991;
                                                                                                                                                                                                                                                                                                                             30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                W09313202-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ51324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ51324 standard; DNA;
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                                                                                                                                                                                                                  1993-227320/28.
DB; AAR44023.
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                                                                                                                                      Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site-directed mutagenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                   sequence coding for the A subunit of the heat labile of a strain of E.coli known to affect humans (Yamamoto Chem., 259, 5037-5044 - see AAQ42768) was subjected
                                                                                                                                                                                                                                                                                                       91IT-0MI3513
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                                                                                                                                                                                                                                                                                                                              92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 304..306
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                                                                                                                                                                                                                                                                                                                                                                                                         /note=
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                         toxin and h
 toxin A subunit sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                              The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51325 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Amino combination cused to introduce the preferred mutation.
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enterotoxigenic bacteria; vaccine; immunogenic detoxified protomer A; site-directed mutagenesis; reduced toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encodes Glu-114 E.coli heat labile toxin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1993
                                                                                                                                                          Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                  enterotoxin
                                                                                                                                                                                             Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                      Domenighini M, Hol
                                                                                                                                                                                                                                                                                                                                             30-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                   P-PSDB; AAR44024.
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                      numbering is based on the cholera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli.
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 BP;
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 236 A;
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Matches:
Conservative:
Mismatches:
Indels:
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 196
                         toxin A subunit sequence)
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 T; 0 other;
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Alignment Scores:

Percent Similarity: Best Local Similarity:

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Matches: Conservative: Mismatches:

711 10 0

Score:

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RESULT 25
AAQ51326
Alignment
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Best Local Similarity:
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                                                   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAQ51314-Q51326). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. Sequence AAQ51326 is a combination of the wild-type coding sequence and the mutagenic primer sequence used to introduce the preferred mutation. (Anino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enterotoxigenic bacteria; vaccine; immunogenic detoxified protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1993
                                                                                                                                                                                                           Immunogenic - useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
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                                                                                                                                                                                                                                                                                                  (BIOC-) BIOCINE
                                                                                                                                                                         Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                               detoxified mutant cholera toxin and heat labile vaccines against infection by Vibrio cholerae ar producing Escherichia coli
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                                                                                                                                                                         and Page 46; 60pp; English.
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Matches:
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Mismatches:
                                                                                                                                                                                                                                                                            Rappuoli
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                                   SEQ1-65T079 (1-15) x AAQ42768 (1-711)
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Best Local Similarity:
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DB:
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                                                                                                                                                                                        of a strain of E.coli known to affect humans. The sequence was published by Yamamoto et al, J.Biol. Chem., 259, 5037-5044.
Mutations at selected positions within this sequence have been to reduce toxicity (see AAQ51314-Q51326). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines protect against attacture in the proteins and their use in vaccines and the sequence was protein and the sequence was sequenced.
                                                                                                                                                          Sequence
                                                                                                                                                                                 protect against
                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                       enterotoxin
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P-PSDB; AAR38728.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enterotoxigenic bacteria; vaccine; immunogenic detoxified LT-A; protomer A; site-directed mutagenesis; reduced toxicity; ADP-ribosyltransferase activity; ss.
                                                                                                                        No.:
                                                                                                                                                                                                                                                                                                                Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                        Domenighini M,
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           SerLeuArgSerAlaHisLeuAlaGlyGln
                                                                                                                                                                                                                                                       sequence encodes the A subunit of the
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711 BP;
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                                                                                            Length:
Matches:
Conservative:
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                                                           Gaps:
                                                                                  Mismatches:
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RESULT 27
AAV81595
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                                                                                                                                           carrier. The antigen may be derived from viruses, bacteria, parasites and fungi or may be tumour antigens, self-antigens and allergens. The compositions are therefore useful in the treatment and prevention of
                                                                                                                                                                                                    prior/subsequent to the antigen, and is preferably administered within a short space of time to the same site; it can also be administered in isolation from antigens as a boost following systemic or mucosal antigen administration. Most preferably, the adjuvant is co-administered with the antigen in the compositions and a pharmaceutically acceptable
                                                                                   e.g. viral diseases, allergic manifestations, diseases caused by pathogens (e.g. bacteria or parasites), AIDS, autoimmune diseases (e.g. Systemic Lupus Erythematosus), Alzheimer's disease and cancers
Sequence 711 BP;
                                                    The adjuvant can also be used to prepare antibodies against selected antigen(s), useful e.g. for diagnostic purposes or for antigen
                                                                                                                                                                                                                                                                                                                                                                                          one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be
                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli heat labile toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenteral adjuvant composition, which comprises the detoxified protein, at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detoxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected antigen e.g. in disease treatment
                                                                                                                                                                                                                                                                                                 the antigen (e.g. by making the antigen more strongly immunogenic or necessitating fewer/lower antigen doses). It can be administered
                                                                                                                                                                                                                                                                                                                                  methods to immunise vertebrate subjects. The adjuvant has the abilit to enhance the humoral and cell-mediated immune responses elicited by
                                                                                                                                                                                                                                                                                                                                                                       (optionally topical) vehicle. The adjuvant comportant administered parenterally in conjunction with at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1A-B; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-070064/06.
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21-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parenteral adjuvant; antigen; antigen; immunisation; humoral cell-mediated immune response; virus; bacterium; parasite; futumour; allergen; pathogen; AIDS; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. coli heat labile toxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV81595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence corresponds to the coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTTGAGAAGTGCTCACTTAGCAGGACAG
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97US-0041227
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 156
G; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region for the A subunit of the
                                                                                                                                                                                                                                                                                                                                                      with at least one antigen in The adjuvant has the ability
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 other;
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Alignment Scores:

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                                  Oligonucleotide 40-mers (AAA51107-26) spanning the entire synthetic CC Escherichia coli heat-labile toxin (LT) A subunit (LT-A) coding sequence CC and a set of complementary 40-mers (AAA51127-46) that centre on the CQ junctions of the coding oligoners allowing 20 bp overlaps were obtained CC commercially and used to construct the synthetic LT-A cDNA. The sequence CC contains plant-preferred codons and elininates sequence motifs CC associated with spurious mRNA processing. A single codon insertion (GTG CC encoding valine) was made to accommodate the creation of a NCOI CC restriction site around the initiator methionine codon. Novel CC polynucleotides encode a mutant LT-A polypeptide or a mutant vibrio CC cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have CC reduced enzyme activity as compared to the wild-type LT-A or CT-A CC polypeptide and where at least one of the codons is altered to a plant CC sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The CC production of transgenic plants to produce edible vaccines, especially craftment against E. coli or V. cholerae. The mutant polypeptides are area of the codons are septial or V. cholerae. The mutant polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ1-65T079 (1-15) x AAV81595 (1-711)
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                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligomer sLT-A For-8 for LT-A cDNA synthesis
                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 2; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-442653/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mason HS, Arntzen CJ;
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(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
- :	8	53.3	263	17	AZ788524	AZ788524 2M0035K08
c 2	8	53.3	418	9	AI347100	Ω
ი ა	8	53.3	424	17	AQ786225	5 HS_31:
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ი 6	8		503	12	BF443144	BF443144 260525 MA
	8	•	535	13	BI343334	371448
8	8		615	17	вн329082	CH230-1
c 9	8		646	12	BG824614	BG824614 602728548
10	8	•	648	17	AZ403745	٠.
c 11	8	•	706	13	BI090511	
12	80		725	17	BH271552	BH271552 CH230-34M
13	80		735	17	вн351398	вн351398 Сн230-175
c 14	8	53.3	768	13	B1658656	BI658656 603283613
15	8	•	790	17	CNS03A1W	AL234653 Tetraodon
_	8		816	17	AQ745347	AQ745347 HS_2276_A
	8	•	829	17	CNS03WYZ	٠.
c 18	8		870	12	BF120183	BF120183 601756489
c 19	8	53.3	884	12	BF575766	BF575766 602135396
20	8	•	967	17	CNS03N3Z	AL251576 Tetraodon
c 21	œ	53.3	1877	11	BC019121	BC019121 Mus muscu

ALIGNMENTS

SOURCE ORGANISM RESULT 1 AZ788524 LOCUS JOURNAL COMMENT FEATURES REFERENCE KEYWORDS VERSION ACCESSION DEFINITION TITLE AUTHORS source Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 263)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0035 row: K column: 08
Seg primer: CACACAGGAAACAGCTATGACC clone UUGC2M0035K08 R, DNA sequence. High quality sequence stop: Location/Qualifiers Unpublished (2000) plasmid inserts Mus musculus AZ788524 263 bp DNA linear GSS 16200035K08R Mouse 10kb plasmid UUGClM library Mus musculus Tel: 801 585 5606 Fax: 801 585 7177 A2788524.1 GI:12928413 house mouse. lass: plasmid ends USA /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" 0.00 20 ŝ 2030 GSS 16-FEB-2001 genomic SLC, S

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RESULT 2
AI347100/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI347100 418 bp mRNA linear EST 30-DEC-19 qp55a12.xl NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926910 3' similar to TR:015498 O15498 SNARE PROTEIN YKT6. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 418)
                                        High quality sequence stop: 1.
Location/Qualifiers
                                                                                                       Trace considered overall poor quality
                                                                                                                                                                                                                                                                                               Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                             Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                       primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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/note="Vector: PWD42nv; Purified genomic DNA from M.
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IMAGE:1926910 3'
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Class: BAC ends
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Mammalia; Eutheria;
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HS_3137_Al_All_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3137 Col=21 Row=A, DNA sequence.
AQ786225
                                                                                                                                                                                                                                                                                                                                           Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3137 row: A column: 21
                                                                                                                                                                                                                                      High quality sequence stop: 424 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keller, A., Shaker, R., Furlong, J., Young, J.,
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S.,
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
1 76 c 83 g 144 t 1 others
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/clone_lib="NCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3137 Col=21 Row=A"
                                                                          /sex="male"
                                                                                                        /clone_lib="CIT Approved Human Genomic Sperm Library D"
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Tissue Procurement: DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tlssue_type="adenocarcinoma cell line"
/tlssue_type="adenocarcinoma cell line"
/lab_host="bH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2:
/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2: xhoI;
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/db_xref="taxon:9606"
/clone="IMAGE:3838221"
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                                                                                                                                                               503 bp mRNA 260525 MARC 2PIG Sus scrofa cDNA 5', mRN BF443144
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 503)

FahrenKrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seatt Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                            pig.
Sus scrofa
                                                                                                                                                  BF443144.1
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Location/Qualifiers
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1 (bases 1 to 490)
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E-Coli DH10B"
a 113 c 99 g 146 t
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/clone="Plate=3240 Col=16 Row=I"
/clone_110="CIT Approved Human Genomic Sperm Library
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                                                                                     Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal R
PO Box 166, Clay Center, NE
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue normal EST discovery in swine Unpublished (2000) Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                            Design and use of two pooled tissue normalized cDNA libraries EST discovery in swine
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                                 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                   stone, R.T., He
and Keele, J.W.
                                                                                                                                                                                                                                                                   1 (bases 1 to 535)
Fahrenkrug, S.C., Fr
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Mammalia; E
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Sus scrofa
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PRimers
                    -minmatch 12 options
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                                                             smith@email.marc.usda.gov
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH329082 615 bp DNA linear GSS 03-DEC-2001 CH230-105p11.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-105p11, DNA sequence.
BH329082
                                                                                                                  Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 105 row: P column: 11
                                                                                                                                                                                                                    Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
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/organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-105P11"
                                                                                 1. .615
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/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9823"
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, Russell,D., Chen,D.,
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; Murinae;
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/clone_lib="CHORI-230 Segment 1"
/sex="Female"

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REFERENCE
AUTHORS
TITLE
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Plate: LLCM1737 row: o column: 12
High quality sequence stop: 639.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information cafond through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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EST.
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                                                                                                               /tissue_type="adenocarcinoma cell line"
/lab_host="DBHOB (phage-resistant)"
/note="Organ: colon; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the labboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
a 172 c 168 g 148 t
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/note="Vector: pTARBAC2.1; Site_1: ECORI; Site_2: ECORI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
171 c 170 g 186 t
                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4868195"
/clone_lib="NIH_MGC_15"
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/db_xref="taxon:9606"
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648 bp DNA linear GSS 03-OCT-200
IM0171010R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0171010 R, DNA sequence.
AZ403745
AZ403745.1 GI:10527758
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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Mammalia; Eutheria;
1 (bases 1 to 648)
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Plate: 0171 row: O column: 10
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
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            125
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="UUGC1M0171010"
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11023 row: e column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BI090511
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Location/Qualifiers
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                                                                                              BI090511 (1-706)
                                                                                                                                                                                                                                            Technologies.
                                                                                                                                                                                                                                                             /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                           /Clone="IMAGE:4996971"
/Clone_lib="NIH_MGC_10"
/Cell_line="MGC36"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Rattus norvegicus
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SEQ1-65T079 (1-15) x BH271552 (1-725)
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                                                                     BH351398 735 bp
CH230-175A4.TJ CHORI-230 Segment 1
CH230-175A4, DNA sequence.
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BH271552 BH271552.1 GI:17183954
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                     вн351398.1
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page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 34 row: M column: 7
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Class: BAC ends.
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Norway rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pTARBAC2.1; Site_1: ECORI; CHORI-230 Rat (BN/SSNHSd/MCW) BAC library Pieter de Jong" a 163 c 181 g 266 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/strain="BN/SSNHsd/MCW"
/db_xref="Itaxon:10116"
/clone="CH230-34M7"
/clone_lib="CHORI-230 Segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
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                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 768)
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Clones are derived from the rat BAC library CHORI-230
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                  BI658656
BI658656.1 GI:15572892
                                                                                                                                                                                                                                                    BI658656 768 bp mRNA linear EST 12-SEP-2001 603283613F1 NCT_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5328074 5',
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Other_GSSs: CH230-175A4.TV
                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                        mRNA sequence.
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment
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 cgapbs-r@mail.nih.gov
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-330 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
171 c 182 g 265 t
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/clone="CH230-175A4"
/clone_11b="CHORI-230 Segment 1"
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SEQ1-65TO79 (1-15) x BI658656 (1-768)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosteni;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

1 (bases 1 to 790)

1 (bases 1 to 790)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,

Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F.,

Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using

Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNS03AlW 790 bp DNA linear GSS 15-MAY-: Tetraodon nigroviridis genome survey sequence T7 end of clone 008B16 of library G from Tetraodon nigroviridis, genomic survey
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished 3 (bases 1 to 790)
                                                                                                      Bouneau, L., Billault, A., Quetier, F., Weissenbach, J.
                                                                                                                                                           2 (bases 1 to 790)
Roest-Crollius, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL234653.1 GI:7893788
GSS; genome survey sequence.
Tetraodon nigroviridis.
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http://image.llnl.gov
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/clone="IMAGE:5328074"
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/dev_stage="5 months"
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Bernot,A. and
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RESULT 16
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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816 bp DNA linear GSS 16-JUL-1999
HS_2276_Al_Bl1_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2276 Col=21 Row=C, DNA sequence.
AQ745347
                                                                                                                                                                                                  Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2276 row: C column: 21
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                                                                                                                                                                    Seq primer: T7
Class: BAC ends
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/note="Genoscope sequence ID : COBG
/note="Genoscope sequence ID : COBG
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E-Coli DH10B"
                                                                 /db_xref="taxon:9606"
/clone="Plate=2276 Col=21 Row=C"
                                                                                                  /organism="Homo sapiens"
                                  /sex="male"
                                              /clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-APR-2000)
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Bernot,A., Fizames,C., Wincker,P., Brottler,P.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                        genome. For more information, please this://www.genoscope.cns.fr/Tetraodon
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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/clone="065M23"
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RESULT 19
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602135396F1
mRNA sequence.
BF575766
BF575766.1 GI:11649478
EST.
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAW9190 row: a column: 23
High quality sequence stop: 651.
Location/Qualifiers
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BF120183.1 GI:10959223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone-"IMAGE: 3985822"
/Clone_lib-"NCI_CGAP_Mam5"
/tissue_type-"tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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8.00
100.00%
100.00%
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                                                                884 bp mRNA linear EST 12-DI NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290670
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CNS03N3Z
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Roest-Crollius,H., Jaillon,O., Dasilva,G., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                              AL251576.1 GI:7972588
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                              Tetraodon nigroviridis genome survey sequence T7 end of c 039\rm K05 of library G from Tetraodon nigroviridis, genomic
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plate: LLCM1133 row: o column: 23
High quality sequence stop: 486.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE.4290670"
/clone="IMAGE.4290670"
/clone="IMAGE.4290670"
/clone="INAGE.4290670"
/clone="ID="NIH_MGC_81"
/lab_host="DH10B (T1 phage-resistant); Vector: pDNR-LIB
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggccgcttgggc); Site_2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAAGGCCGAGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, G, or T). A Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
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                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbort Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus, clone IMAGE:5002987, mRNA.
BC019121
BC019121 GI:17403065
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Web site: http://www.nisc.nih.gov/
COOHact: nisc_mgc@nhgri.nih.gov
Akhter,N. Ayele,K. Beckstrom-Sternberg,S.M.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkl
                                                                                                                                                                                                                                                                            Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Direct Submission
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                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                Gaithersburg, Maryland,
                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="039K05"
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/note="Genoscope sequence ID : COBG039AF03LP1~end : T7"
/ 203 c 245 g 246 t 1 others
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Brinkley,C., Brook
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  Brooks, S.,
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Search completed: January 28, Job time: 1272.67 secs
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                                                                                                                                                                 SEQ1-65T079 (1-15) x BC019121 (1-1877)
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                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
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                                                                                                                                                                                                                                                Best Local Similarity:
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                                                                                 353 AGCCTGAGGTCTGCACACTTGGCG 330
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                                                                                                       SerLeuArgSerAlaHisLeuAla 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 39 Row: c Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identity to protein
This clone has the following
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                473
                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mammary tumor. M old mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam2" /lab_host="DH10B" /note="Vector: pCMV-SPORT6" a 504 c 525 g 375 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:5002987"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/map="FVB/N-3"
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                     2003, 13:16:52
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Conservative:
Mismatches:
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TITLE OF INVENTION: Immunogenic Detoxified Mutants of TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation TITLE OF INVENTION: Their Use for the Preparation of Vaccines NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

and

STREET: 4560 Hort CITY: Emeryville STATE: California

California

USA

ADDRESSEE:

E: Chiron Corporation 4560 Horton Street

APPLICANT:

Pizza, Mariagrazia

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GenCore version 5.1.3 Compugen Ltd
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OM protein - nucleic search, using frame_plus_p2n model Run on: January 28, 2003, 10:38:10 ; Search time 54 Seconds (without alignments) 85.188 Million cell updates/sec

Sequence: Perfect score: Title: Scoring table: OLIGO SEQ1-65T079 SLRSAHLAGQSILSG 15

Searched: Xgapop 60.0 Ygapop 60.0 Fgapop 6.0 Delop 6.0 441362 seqs, 153338381 residues Xgapext Ygapext Fgapext Delext 60.0 60.0 7.0 7.0

8

Minimum DB Maximum DB Total number of hits satisfying chosen seq length: 0 seq length: 2000000000 parameters:

Post-processing: Listing first 1000 summaries

Command line parameters:
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-D8-Issued_Patents_NA -QFMT-fastap -SUFFIX=011p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=011g0 -TRANS-human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE=LOCAL
-USTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-BORIN682_@CGN_1 1_25_grunat_23012003_130141_7891 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=60 -XGAPEXT=60 -FGAPEXT=7
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Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ъ	Result
10	sult Query No. Score Match Length DB ID
10 66.7	Query Match
711	Length
ω	- BB
711 3 US-08-823-120-5	esult Query NO. Score Match Length DB ID Description
Sequence 5, Appli	Description

ALIGNMENTS

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RESULT 1
US-08-823-120-5
                              Sequence 5, Application US/08823120 Patent No. 6149919 GENERAL INFORMATION:
 APPLICANT:
Domenighini, Mario
Rappuoli, Rino
```

Ş Search completed: January 28, 2003, 13:19:48 Job time: 54 secs Best Local Similarity: Query Match: SEQ1-65TO79 (1-15) x US-08-823-120-5 Score: Alignment Scores: US-08-823-120-5 Percent Similarity: TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2708
TELEFAX: (510 (655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic) CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08
APPLICATION NUMBER: US 08
FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,1
REFERENCE/DOCKET NUMBER: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk FEATURE: NO : : 190 AGTTTGAGAAGTGCTCACTTAGCAGGACAG 219 COUNTRY: 2IP: 946 FILING DATE: NAME/KEY: LOCATION: 1 SerLeuArgSerAlaHisLeuAlaGlyGln 10 94608-2916 0.0182 10.00 100.00% 100.00% 66.67% US 08/256,003 G 0315.001 (1-711)Gaps: Length: Matches: Indels: Mismatches: Conservative: 711 10 0 0

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Command line parameters:

-MODEL-frame+_D2n.model -DEV-xlh
-O_cgp2_1/USETO_spool_MORING82/runat_23012003_130142_7908/app_guery.fasta_1.597
-OB-Published_Applications_NA -QFMT=fastap -SUFFIX=olip2n.rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
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-MAXLEN-200000000 -USER-BORIN682_@CGN_1_133_@runat_23012003_130142_7908
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-FGAPEXT=7 -YGAPOP=60 -YGAPPEXT=60 -DELEXT=7
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Perfect score:
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                                                Score
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Ygapop 60.0 , Ygapext 6
Fgapop 6.0 , Fgapext
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Match Length DB ID
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Sequence 5, Appli
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ALIGNMENTS

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Best Local Similarity:
Query Match:
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Search completed: January 28, 2003, 13:23:11 Job time: 63 secs
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                                                                                                                                                                                                                                                                               ; LENGTH: 723
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-950-335A-5
                                                                                                                        SEQ1-65TO79 (1-15) x US-09-950-335A-5 (1-723)
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                                                                                                                                                                                                                                                 Alignment Scores:
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TITLE OF INVENTION: GENETICALLY ENGINEERED CO-EXPRESSION DNA VACCINES, CONSTRUCTIO TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 4115-128

CURRENT APPLICATION NUMBER: US/09/950,335A

CURRENT FILING DATE: 201-09-10

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.1

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09950335A Publication No. US20020193330A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Matches:
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Indels:
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Command line parameters:
-MODEL-frame+_p2n.model -DEV=xlh
-MODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPT0_spool/BORIN682/runat_23012003_130141_7873/app_query.fasta_1.597
-DB-GenEmbl -QFMT=fastap -SUFFIX=olip2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE=LOCAL -OUTEMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN-2000000000
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-WARRI_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Fgapop 6.0 , F
Delop 6.0 , D
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285.757 Million cell updates/sec
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Pickett,C.L., Weinstein,D.L. and Holmes,R.K.

Genetics of type IIa heat-labile enterotoxin of Escherichia coli:
operon fusions, nucleotide sequence, and hybridization studies
D. Bacteriol. 169 (11), 5180-5187 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M17894.1 GI:146671
enterotoxin; heat-labile enterotoxin.
E.coli (strain SA53) DNA.
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E.coli heat-labile
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53.3 229289
/translation="MSSKKIIGAFVLMTGILSGQVYAGVSEHFRNICNQTTADIVAGV
QLKKYIADVNTNTRGIYVVSNTGGVWYIPGGRDYPDNFLSGEIRKTAMAAILSDTKVN
                                                                                                                       829.
                                                                                                                                                 /protein_id="AAA24093.1"
/protein_id="AAA24093.1"
/db_xref="GI:446672"
/translation="MIKHVLLFFVFISFSVSANDFFRADSRTPDEIRRAGGLLPRGQQ
/translation="MIKHVLLFFVFISFSVSANDFFRADSRTPDEIRRAGGLLPRGQQ
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VVAPAPNLFDVNGVLGRYSPYPSENFPAWREMPWSTFAPEGCVPNNKEFKGGVCISA
YRGDLFRGLTYAPNEDGYQLAGFFSNFPAWREMPWSTFAPEGCVPNNKEFKGGVCISA
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                                /transl_table=11
/protein_id="AAA24094.1"
/db_xref="GI:146673"
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                                                                                                                                        TNVLSKYDLMNFKKLLKRRLALTFFMSEDDFIGVHGERDEL"
                                                                                                                                                                                                                                                                                                                               /organism="Escherichia
/db_xref="taxon:562"
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                                                                                   /codon_start=1
                                                                                                   /note="heat labile enterotoxin type IIa B"
                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                               /note="heat labile enterotoxin type IIa
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BASE COUNT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Accombridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Accombridgeshire, CB10 1SA, UK. E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-100P23 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt SWISSPROT;\ Tr:,\ TREMBL;\ wp:,\ WORMPEP;\ Information\ on\ the\ WORMPEP\ database\ can\ be\ found\ at\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL603842 229289 bp DNA linear ROD 17-Mouse DNA sequence from clone RP23-100P23 on chromosome 11,
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/note="Single clone region. Sequence from clone PCR only." 170770. .170774
/note="1327 bases of IS2 transposon (V00610) removed here. This sequence represents the duplicated flanking sequence
                                                                                                                                           /note="Sequence from uni-directional dGTP big dye terminator reads only." 125096. 125397
                                                                                                                                                                                                                                                                     59782.
                                                                                                                                                                                                                                                                                                  /clone="RP23-100P23"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/note="Sequence from uni-directional dGTP big dye terminator reads only."
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Command line parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -Qc/cgn2_1/USPTO_Spool/BORIN682/runat_23012003_130140_7866/app_query.fasta_1.597
-Dbs-N_Geneseq_101002 -QFWT=fastap -SUFFIX=011P2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-blts -START=1 -END--1 -MATRIX-011g0 -TRANS-human40.cd1
-LIST=1000 -DCCALIGN=200 -THR_SCORE-quality -THR_MIN=8 -ALIGN=50 -MODE-LOCAL
-OUTEMT=pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-BORIN682_@CGN_1_1_187_@runat_23012003_130140_7866 -NCPU=3
-USER-BORIN682_@CGN_1_1_187_@runat_23012003_130140_7866 -NCPU=6 -ICPU-3
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-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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      N_Geneseq_101002:*

1: SIDS2/gcgdata/
2: SIDS2/gcgdata/
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Ygapop 60.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2185239 seqs, 1125999159 residues
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15
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID

Description

No matches found

Search completed: January 28, 2003, 10:56:27 Job time: 344.333 secs

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Minimum
Maximum
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-DB=EST -OFMT=fastap -SUFFIX=011p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=011g0 -TRANS=human40.cdi -LIST=1000
-DCCALIGN=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_XLPXY -NO_MMP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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Fgapop
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191.185 Million cell updates/sec
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gb_est1:*
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gb_htc:*
                      em_gss_mus:*
em_gss_other:*
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          em_gss_pro:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Lute Lute Suga Suga M. a M.	Ok. Ok. Tag Tag Ok. ES	MUSCULUS CDNA Clone 4930563A03 3', mRNA sequen VERSION BB016585 GI:16257466 KEYWORDS SOURCE ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalla; Eutheria; Rodentia; Sciurognathi; Mu REFERENCE AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M.,	ALIGNMENTS 683 bp mRNA RIKEN full-length enriched, adv	Result Query No. Score Match Length DB ID 1 8 53.3 683 10 BB016585
kohama Institute kohama Institute I and Chemical Research (RIKEN) umi-ku, Yokohama, Kanagawa 230-0045, Japan ken.go.jp, ken.go.jp/ Hayatsu,N., Sugahara,Y., Shibata,K., Itoh , Muramatsu,M. and Hayashizaki,Y. action of cap-trapper-selected cDNAs to libraries for rapid discovery of new (10), 1617-1630 (2000) noue,K., Togawa,Y., Izawa,M., Ohara,E., IShikawa,T., Ozawa,K., Tanaka,T., Matsuura , Muramatsu,M., Inoue,Y., Kira,A. and ce analysis (RISA) system384-format 384 multicapillary sequencer. Genome Res.) Shibata,K., Itoh,M., Carninci,P., Sugahara	onr hnc anc Su , T	uteleosto Murinae; ki,T., Ha	NTS mRNA linear EST 18-OCT-2001 ched, adult male testis (DH10B) Mus	Description BB016585 BB016585

cDNA library was prepared and sequenced in Encyclopedia Project of Genome Exploration Genomic Sciences Center and Genome Science

Mouse Genome Research Group in Riken Laboratory in RIKEN.

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with

Computational Sequences Mamm. Genome. 12, 673-677 (2001)

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Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: January 28, 2003, 13:16:52 Job time : 1270.67 secs
                                     В
                                                       Qy
                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                         SEQ3-65T079 (1-15) x BB016585 (1-683)
                                                                                                                                  Score:
                                                                                                                                         Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                   Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                              223
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930563A03"
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                                                                                                                                                                                                                                                                                                                                                                                 (DH10B)"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, adult male testis
                                                                                           11.2
8.00
100.00%
100.00%
53.33%
                                                                                                                      Length:
Matches:
Conservative:
                                                                                         Gaps:
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Indels:
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Search completed: January 28, 2003, 13:19:48 Job time: 54 secs
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No.
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-DB=1ssued_Patents_NA -QFMT=fastap -SUFFIX=01ip2n.rni -MINNATCH=0.1 -LOOPCL=0
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-NO_XLPXY -NO_MNAP -LARGOUGRY -NGE_SCORES=0 -NAIT -LONGLOG -DEY_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELCP=6 -DELEXT=7
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Perfect score:
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-MODEL-frame+_p2n.model -DEV-x1h
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                 No matches found
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                                                                                                                                                                                                        Score
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441362 segs, 153338381 residues
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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GenCore version 5.1.3 Compugen Ltd

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Result
No.
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-QB-Published_Applications_NA -QFMT=fastap -SUFFIX-olip2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-oligo
-TRANS-human40.cd1 -LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=8
-ALIGN=50 -MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=BORIM682_@CGN_1_1_33_@runat_23012003_130142_7908
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARR_TIMEOUT=30 -THREADS=1 -XCAPOP=60 -XCAPEXT=60 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlh
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Maximum DB seq length: 2000000000
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                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
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6:
7:
9:
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11:
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      Query
Match Length DB
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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15
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                                                                                                                                                                                                                                                                     // Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq: *
// Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq: *
// Cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
// Cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq: *
// Cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *
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106.968 Million cell updates/sec
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Description
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No matches found

Search completed: January 28, 2003, 13:23:11 Job time : 63 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV-x1h

-MODEL-frame+_p2n.model -DEV-x1h

-Q-cgn2_1/USPTO_Spool/BORIM682/runat_23012003_130141_7873/app_query.fasta_1.597

-DB-GenEmb1 -QFMT-fastap -SUFFIX-011p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS-bits -STARP-1 -END--1 -MATRIX=0.11go -TRANS-human40.cdi -LIST=1000

-DOCALIGN=200 -THR_SCORE-quality -THR_MIN-8 -ALIGN=50 -MODE-LOCAL -OUTFMT-pto

-NORM-ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USER-BDRIN682_@CGN_1_1_2425_@runat_23012003_130141_7873 -NCPU=6 -ICPU=3

-NO_XLPXY -NO_MMAP -LARGEQUERY -NEC_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOXT=7

-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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DB seq length: 2000000000
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1 REFNSLPNNK
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Ygapop 60.
Fgapop 6.
Delop 6.
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gb_ph:*
gb_pr:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_nln:*
35: em_htg_roi:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
40: em_htgo_nus:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.

Score

Oberty Match Length DB ID Description Match Length DB ID Description 66.7 1262 1 ECOETOXHL 53.3 635 10 AF204796SB AF204403 Mus muscu 53.3 71402 2 AC1237SB Mus muscu 53.3 101445 9 AL133411 AL133411 Human DNA 53.3 114928 2 AC125479 AC125479 AC125479 AC125439 AC025453 Homo sapi 53.3 145882 2 AL139131 Homo sapi AL139131 Homo sapi 53.3 155394 2 AC0213881 AC012844 Homo sapi 53.3 154455 2 AC02328 AC02328 Homo sapi 53.3 176123 9 AL390718 AC025445 Homo sapi 53.3 184635 9 AC026445 Homo sapi 53.3 184635 9 AC026445 Homo sapi 53.3 184635 9 AC

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ALIGNMENTS

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CDS	-10 signal	-35_signal	gene				source	FEATURES	COMMENT	PUBMED	MEDLINE	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	ECOETOXHL	1
			11262	/db_xrer= caxon:30z /clone="pcP4185"	/strain="41"	/organism≖"Escherichia coli"	11262	Ò	On Nov 28, 1994 this sequence version replaced gi:341953.	2670900	89359131	J. Bacteriol. 171 (9), 4945-4952 (1989)	IIb heat-labile enterotoxin gene of Escherichia coli	Cloning, nucleotide sequence, and hybridization studies of the type	Pickett, C.L., Twiddy, E.M., Coker, C. and Holmes, R.K.	1 (bases 1 to 1262)	Escherichia.	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	Escherichia coli		LT-IIb gene; enterotoxin type IIb.	M28523.1 GI:576584	M28523	(LT-IIb) A and B chain genes, complete cds.	heat-labile en	ECOETOXHL 1262 bp DNA linear BCT 18-NOV-1994		

TITLE

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ4-65T079 (1-15) x ECOETOXHL (1-1262)
                    REFERENCE
                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                        SEGMENT
                                                                                                                                                                                                                                                                                                                                                 AF204796S8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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                                 MEDLINE
PUBMED
                                                                                                           AUTHORS
TITLE
                                                                       JOURNAL
 AUTHORS
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                                                                                            CDNA
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammaalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 635)
                                                                                                                                                                                                                                                                                            Mus musculus lanosterol AF204803
Debeljak,N., Horvat,S.,
                                                                       Pflugers Arch. 439 (3 Suppl), R7-R8 (2000)
                                                                                                         Debeljak, N., Horvat, S., Komel, R. and Rozman, D. Molecular cloning and partial characterisation
                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                      8 of 9
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                (bases 1 to 635)
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173. .901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAA53285.1"
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/translation="MAKYISFFISLFLISFPLYANDYFRADSRTPDEVRRSGGLIPRG
ODEAYERGTPININLYDHARGTATGNTRYNDGYVSTTTTLRQAHLLGQNMLGGYNEYY
IYVVAAAPNLEDVNGVLGRYSDYPSENEYAALGGIPLSQIIGWYRVSFGAIEGGMHRN
RDYRRDLFRGLSAAPNEDGYRIAGFPDGFPAWEEVPWREFAPNSCLPNNKASSDTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="LT-
963. .1259
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ELTKYISDINNNTDGMYVVSSTGGVWRISRAKDYPDNVMTAEMRKIAMAAVLSGMRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="enterotoxin"
/protein_id="AAA53286.1"
/db_xref="GI:576586"
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/product="enterotoxin"
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/note="B chain of heat-labile
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/note="A chain of heat-labile enterotoxin type IIb"
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                                                                                                                                                                                                                                                                                                        635 bp DNA linear ROD 30-APR-200 14-alpha-demethylase (CYP51) gene, exon 9.
Vouk, K., Lee, M. and Rozman, D.
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Conservative:
Mismatches:
Indels:
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Murinae; Mus
                                                                                                         mouse Cyp51
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JOURNAL REFERENCE
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               Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarate, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Leither, M., Marchis, N., March
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 71402)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-453L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71402 bp DNA Mus musculus clone RP23-453L19, LOW-PASS AC123728
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Submitted (15-NOV-1999) Medical Center for Molecular Biology,
Institute of Biochemistry, Medical Faculty, University of
Ljubljana, Vrazov trg. 2, Ljubljana 1000, Slovenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization of the mouse lanosterol l4alpha-demethylase (CYP51), a new member of the evolutionarily most conserved cytochrome P450 family Arch. Biochem. Biophys. 379 (1), 37-45 (2000)
                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC123728.2 GI:21427923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
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515. .>635
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/strain="129/Sv"
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1. .635
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McCarthy, M., McEwan, P.,
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McKernan, K., Meldrim, J.,
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REFERENCE

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Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange Indmann, A., Talamas, J., Tesfaye, S., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schubback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
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Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Nell,D., Ollver,J., Peterson,K., Phunkhang,P., Plerre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Pollara,V., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
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Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,
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Anderson, S., Barna, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This record contains 87 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                  100 bp
1556: contig of 729 bp it.
1557 1656: gap of 100 bp
1657 2387: contig of 731 bp in
2388 2487: gap of 100 bp
3228: contig of 3328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project Information Center project name: L26488 Center clone name: 453_L_19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
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           4155:
                            3228: contig of 741 bp 10
328: gap of 100 bn
4055: con++-
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                                                                                                                                               Submitted (17-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Mar 21, 2002 this sequence version replaced gi:10931831. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                     only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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169 41299; contig of 731 bp in length
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DB: Query

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SEQ4-65T079 (1-15) x AL133411 (1-101445)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCAACTCCCTACCCAACAACAAA 95182
Direct Submission
Submitted (27-UN-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-57P14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
                                                                                                          Shaull, S., Lin, S., Dixon, R., Cook, D., Kim, D. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC125479 114928 bp DNA linear Medicago truncatula clone mth1-7f11, WORKING DRAFT
                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                 Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone
                                                                                                                                                                                                                                                                           Shaull, S., Lin, S., Dixon, R.,
                                                                                                                                                                                                                                                                                                                                          Medicago.
                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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The true left end of clone RP11-298E2 is at 99446 in this sequence
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RP11-57P14 It may be shorter because we sequence overlapping
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VECTOR: pBACe3.6
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/chromosome="9"
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/clone_lib="RPCI-11.1"
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                                                                                                                                       Gonzales, B.,
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                       Room 208, Norman,
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RESULT 6
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                                                                                                                                                                        KEYWORDS
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TITLE
JOURNAL
                                            AUTHORS
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1 3787: contig of 3787 bp in length

3788 3887: gap of unknown length

1362: la261: gap of unknown length

1362: la261: gap of unknown length

23764: contig of 10503 bp in length

23765: 23864: gap of unknown length

23865: 37301: contig of 13437 bp in length

37302: 37401: gap of unknown length

37402: 51846: contig of 13437 bp in length

51947: 51946: gap of unknown length

51947: 51946: gap of unknown length

51947: 51946: gap of unknown length

73673: 3772: gap of unknown length

73673: 3772: gap of unknown length

73673: 3772: gap of unknown length

73673: 114928: contig of 41156 bp in length
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On Aug 19, 2002 this sequence version replaced g1:22138503
Unpublished
                      Sequencing of Human Chromosome
                                            DOE Joint Genome Institute.
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 142959)
                                                                                                                                                                                            AC025453
AC025453.5 GI:13677022
                                                                                                                                                                                                                                                      AC025453 142959 bp DNA linear Homo sapiens chromosome 5 clone CTD-2150A8, WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                            Homo sapiens
                                                                                                                                                Homo sapiens.
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This sequence will be replaced by the finished sequence as so
                                                                                                                                                                                                                                  ordered pieces.
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/db_xref="taxon:3880"
/clone="mth1-7f11"
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DRAFT SEQUENCE,
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                                                           Db 139734
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SEQ4-65TO79 (1-15) x AC025453 (1-142959)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 138699 bases at least Q40
Consensus quality: 141252 bases at least Q30
Consensus quality: 141205 bases at least Q30
Consensus quality: 141200 bases at least Q30
Estimated insert size: 155560; agarose-fp estimation
Quality coverage: 5.9 in Q20 bases; agarose-fp estimation
Quality coverage: 5.9 in Q20 bases; agarose-fp estimation
** NOTE: This is a 'working draft' sequence. It currently
** consists of 8 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
** This converse...**

** This converse...**

** This is a 'working draft' sequence. It currently

** are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

** of the gaps between them are based on estimates that have
TTTAACTCTTTGCCTAATAACAAG 139711
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1 5661 contig of 5661 bp in length
5662 5761 gap of unknown length bp in 23815 gap of unknown length
23816 83941 contig of 60126 bp in length
83942 84041 gap of unknown length
84042 97947 contig of 13906 bp in length
97948 98047 gap of unknown length
97948 104249 contig of 6202 bp in length
104350 106391 contig of 6202 bp in length
104350 106391 contig of 2542 bp in length
106892 135029 contig of 28038 bp in length
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DOE Joint Genome Institute.
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er: Joint Genome Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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26024 c 25587 g 43364 t 704 other
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   misc_feature
                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 110% of reads
Chemistry: Dye-terminator Big Dye; 110% of reads
Consensus quality: 137751 bases at least Q40
Consensus quality: 140505 bases at least Q30
Consensus quality: 14252 bases at least Q30
Consensus quality: 14252 bases at least Q20
Insert size: 144882; sum-of-contigs
Insert size: 156750; 4.8% error; agarose-fp
Quality coverage: 3.78x in Q20 bases; sum-of-contigs Quality
coverage: 3.58x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 11, 2000 this sequence version replaced gi:9212172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145882 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome 1 clone RP11-172P10, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                            56578 56677: gap of 100 bp 56678 66988: contig of 10311 bp in length 66989 67088: gap of 100 bp 67089 69189: contig of 2101 bp in length 69190 69289: gap of 100 bp in length 69290 103697: contig of 34408 bp in length 103698 103797: gap of 100 bp 103798 116670: contig of 12873 bp in length 11671 116770: gap of 100 bp 116771 131840: contig of 15070 bp in length 11671 131840: contig of 15070 bp in length
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l31941 145882: conti
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28659 28758: gap of 100 bp

28759 33908: contig of 5150 bp in length

33909 34008: gap of 100 bp

34009 37706: contig of 3698 bp in length

37707 37806: gap of 100 bp

57807 57807: Config of 13091 bp in length
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                            /clone="RP11-172P10"
/clone_lib="RPCI-11.1"
                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                Location/Qualifiers
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contig of 13942 b
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               Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Deuthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garper, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garper, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garper, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garper, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garper, T., Garza, N., Gall, R., Gabisi, A., Gao, J., Garcia, A., Garper, T., Garza, N., Gall, R., Gabisi, A., Gao, J., Garcia, A., Garper, T., Garza, N., Gall, R., Gabis, A., Garper, T., Garza, N., Gall, R., Garber, T., Garza, N., Garber, T., Garza, M., Garber, T., Garza
                                                                                                                                                                                                                                                                                               Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryan Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                                                           Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bo
Gorrell, J.H., Guevara, W., Gunaratne, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
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131941. .145882
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67089. .69189
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28759. .33908
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116771. .131840
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103798. .116670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 152617)
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Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 47 contlys. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 118622 bases at least Q40
Consensus quality: 122734 bases at least Q30
Consensus quality: 125850 bases at least Q20
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Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 152020 bases at least Q40
Consensus quality: 152947 bases at least Q30
                                                                                                                                                                                                                                        Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Apr 11, 2000 this sequence version replaced gi:7523912.
                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 154455)
Waterston, R.H.
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                                                                                                                             Center project name: H_NH0015D23
                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
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/db_xref="taxon:10116"
/clone="CH230-33965"
/ 31543 c 31335 g 40206 t
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99172: gap of unknown le
103575: contig of 4003 bp
103675: gap of unknown le
112734: contig of 9059 bp
112834: gap of unknown le
112742: contig of 6908 bp
119742: contig of 6908 bp
119842: gap of unknown le
129603: contig of 9761 bp
129703: gap of unknown le
138726: contig of 9761 bp
138726: contig of 13791 b
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                Sequencing of Human Chromosome Unpublished
                                                        1 (bases 1 to 155394)
DOE Joint Genome Institute.
                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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(bases 1 to 155394)
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98643. .154455
/note="assembly_name:Contig6
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/chromosome="5"
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10735: gap of unknown length
44171: contig of 33436 bp in le
44271: gap of unknown length
9842: contig of 54271 bp in le
98642: gap of unknown length
154455: contig of 55813 bp in le
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
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Direct Submission Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                  Wallis,J
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 176123)
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/clone_lib="RPCI human BAC library 11"
28012 c 28437 g 52363 t 100 others
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/db_xref="taxon:9606"
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25917: gap of unknown length
155394: contig of 129477 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on Nov 16, 2001 this sequence version replaced gi:16444706. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RP11-502H18 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-502H18 is at 1 in this sequence. The true left end of clone RP5-1180Cl0 is at 155124 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                   1 (bases 1 to 184635)
DOE Joint Genome Institute
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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RP11-502H18 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                          Homo sapiens
                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone
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/db_xref="taxon:9606"
/chromosome="1"
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/clone_lib="RPCI-11.2"
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                                                        Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Thang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                  Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 192263)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 6, 2001 this sequence version replaced gi:10567849. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-OCT-2000) DOE Joint Genome Drive, Walnut Creek, CA 94598, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-MAY-2000) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 192263)
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Center clone name: 098L05
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                                                                                                                                                                                                                                                                                                                                /note="bacterial transposon excised; IS1 element sequence can be found in GenBank Accession Number AE000112.1 nucleotides 9258-10025; 768 bp"

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AC068665 (nucleotides 199679-205937) clone RP23-426K16
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/chromosome="5"
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/strain="C57BL6/J"
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GenCore version 5.1.3 Compugen Ltd.

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Minimum DB :
Maximum DB :
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-Qs-/Ggn2_1/USPTQ_Spool/Borin6827.runat_23012003_130140_7866/app_query.fasta_1.597
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=011p0 .rng -MINMATCH=0.1 .LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=011p0 -TRANS=human40.cdi
-LIST=1000 -DCCALIGN=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE=LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_SER=BORIN682_eCGN_1_1_197_erunat_23012003_130140_7866 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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-MODEL-frame+_p2n.model -DEV-xlh
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                   January 28, 2003, 10:32:26; Search time 344.333 Seconds (without alignments) 98.103 Million cell updates/sec
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15
JSIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

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SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*

SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*

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SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA198.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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Ygapext 60.0
Fgapext 7.0
Delext 7.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query No. Score Match Length DB ID Description

No matches found

Search completed: January 28, 2003, 10:56:27 Job time: 344.333 secs

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-/Cgn2_1/USTTO_spool/BORIN082/runat_23012003_130141_7880/app_query.fasta_1.597
-Q-/Cgn2_1/USTTO_spool/BORIN082/runat_23012003_130141_7880/app_query.fasta_1.597
-DB=EST -QFMT=fastap -SUFFIX=011p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blts -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-UCALIGN=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE-LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=BORIN682_@CGN_1_1349_@runat_23012003_130141_7880 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARCEQUERY -NUS_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7 Word Minimum DB Maximum DB Database Total number of hits satisfying Searched: Scoring table: Perfect score: Title: Run on: OM protein - nucleic search, using frame_plus_p2n model Post-processing: Listing first 1000 summaries size: .. seq length:
seq length: Xgapop 60.0 Ygapop 60.0 Fgapop 6.0 Delop 6.0 8 OLIGO 16154066 seqs, 8097743376 residues SEQ4-65T079 January 28, REFNSLPNNKASSDT em_htc:*
gb_est1:* em_estpl:*
em_estro:* em_estmu:*
em_estov:* em_gss_other:*
em_gss_pro:*
em_gss_rod:* em_gss_hum: *
em_gss_inv: *
em_gss_pln: * em_gss_vrt:*
em_gss_fun:*
em_gss_mam:* gb_est2:*
gb_htc:* em_estin:* em_esthum:* em_estba:* em_gss_mus:* gb_gss:* em_estom:* em_estfun:* gb_est5:* gb_est4:* gb_est3:* 2000000000 2003, 10:36:45; Search time 1270.67 Seconds (without alignments)
191.185 Million cell updates/sec Xgapext Ygapext Fgapext Delext chosen 15 60.0 7.0 7.0 parameters: 6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

BASE COUNT 73	University of Asmundson Haller 1-(530)-Fax: 1-(530)-Email: akozik belongs to confor details. FEATURES Plate: QGF11 FEATURES 1	REFERENCE 1 (bases AUTHORS Lin, H., Va , P., Kolten TITLE Lettuce an http://com JOURNAL Unpublishe COMMENT Department	RESULT 1 BQ987313/C LOCUS DEFINITION QGF11N24.y ACCESSION BQ987313 VERSION BQ987313.1 KEYWORDS EST. SOURCE Lactuca sa ORGANISM Lactuca sa Eukarryota; Spermatoph Asteridae;	Result Query No. Score Match C 1 8 53.3 C 2 8 53.3 C 4 8 53.3 C 4 8 53.3 C 4 8 53.3 C 5 8 53.3 C 5 8 53.3
/Cultivara Lacous 236 / Cultivara Lacous 2436 / Cultivara 2436 / Cultivar	of California at Davis (UCD) Hall, UCD, Davis, CA 95616, USA 0)-742-1742 0)-752-9659 21k@atgc.org (michelmore@vegmail.ucd contig QG_CA_Contig126, see http:// 5, 11 row: N column: 24. 1270_"Ifficial Satisface."	l (bases 1 to 270) 1 (bases 2 to 270) 1 (bases 1 to 270) 2 (bas	BQ987313 270 bp mRNA linear EST 21-AUG-2002 QGF11N24.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGF11N24, mRNA sequence. BQ987313 BQ987313.1 GI:22404838 EST. Lactuca sativa. Lactuca sativa. Lactuca sativa. Lactuca sativa. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; magnoliophyta; Asteraceae; Lactuceae; Tactuca;	Pary Length DB ID Description 1.3 270 14 BQ987313 BQ987313 QGF11N24. 1.3 282 14 BQ986290 BQ986290 QGE9B01.7 1.3 343 14 BQ983106 BQ983106 QGE18D17. 1.3 501 14 BU010453 BU010453 QGJ13H21. 1.3 597 17 FR0048612 AL604421 Fugu rubr 1.3 763 17 AZ698405 AZ698405 RPCI-23-2 1.4 BU010453 ALGNMENTS

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REFERENCE
AUTHORS
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BQ986290/c
LOCUS
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KEYWORDS
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Best Local Similarity:
Query Match:
                            Pred. No.:
                                                    Alignment Scores:
                                                                                               ORIGIN
                                                                                                                       BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nttp://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases 1 to 264)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactuca sativa
Lactuca y Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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QGE9B01.yg.ab1 QG_EFGHJ lettuce
QGE9B01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for details.

Plate: QGE9 row: B column: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elli, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   belongs to contig QG_CA_Contig126,
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                                                                                                                                                                                                     Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                       TAG_TISSUE=germinating seeds
TAG_SEQ=TCTGTGCGGG"
                                                                                                                                                                                     TAG_LIB=QG_EFGHJ lettuce serriola
                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBrcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGE9B01"
                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
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                                                                                                                    93 t
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    282
8
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BQ983106/c
                                             Percent Similarity:
Best Local Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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Lettuce and Sunflower ESTs from the Compositae Genome Project
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Plate: QGE18 row: D
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Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
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48 c 82 g
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TAG_LIB=QG_EFGHJ lettuce serriola
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/lab_host="E.coli"
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/cultivar="L.serriola"
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Wed Jan 29 10:46:39 2003

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                     LeuProAsnAsnLysAlaSerSer 13
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QGJ13H21.yg.abl QG_EFGHJ L
QGJ13H21, mRNA sequence.
BU010453
BU010453.1 GI:22444848
EST.
 Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellis
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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singleton, see http://cgpdb.ucdavis.edu/ for details.
plate: QGJ13 row: H column: 21.
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QGJ13H21"
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/lab_host="E.coli"
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SEQ4-65TO79 (1-15) x FR0048612 (1-597)
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                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 763)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, and Traco, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, and Traco, M.
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                          and Fraser,C.M.
Mouse BAC End Sequences from
Unpublished (1999)
Other_GSSs: RPCI-23-240L10.TV
                                                                                                                                                                                                                                                                                                                                                                              AZ698405 763 bp DNA linear GSS 24-JAN-2001 RPCI-23-240L10.TJ RPCI-23 Mus musculus genomic clone RPCI-23-240L10
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Vector: pBluescript II KS
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1 (bases 1 to 597)
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GSS sequence, clone C057B06aC3, genomic survey
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Conservative:
Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
Search completed: January 28, 2003, 13:16:53 Job time: 1271.67 secs
                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                            SEQ4-65T079 (1-15) x AZ698405 (1-763)
                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                             Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 240 row: L column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                     246
                                                                                                                                                                                                                                                                                                                                                                                     മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-240L10"
/clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                           /note="organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "a 160 c 148 g 209 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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                                                                                                                                                                                                      154
8.00
100.00%
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53.33%
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8
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В ρ

DB:

Score:

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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlh
-MODEL-frame+_p2n.model -DEV-xlh
-O_ccgn2_1/USBTO_Spool_MORINN82/runat_23012003_130141_7891/app_query.fasta_1.597
-DB-Issued_Patents_NA -OFMT-fastap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -STARF=1 -END=-1 -MATRIX=olip0 -TRANS=human40.cdi
-LIST=1000 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=8 -ALIGN=50 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-BORIN682_@CGN_1_1_25_@runat_23012003_130141_7891 -NCPU-6 -TCPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NG_SCORES=0 -WARIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOD=60 -XGAPEXT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXI=7
                                                                                   Result
No.
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 1000 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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No matches found
                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                   Score Match Length DB
                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*

1: /cgn2_6/ptodata/2

2: /cgn2_6/ptodata/3

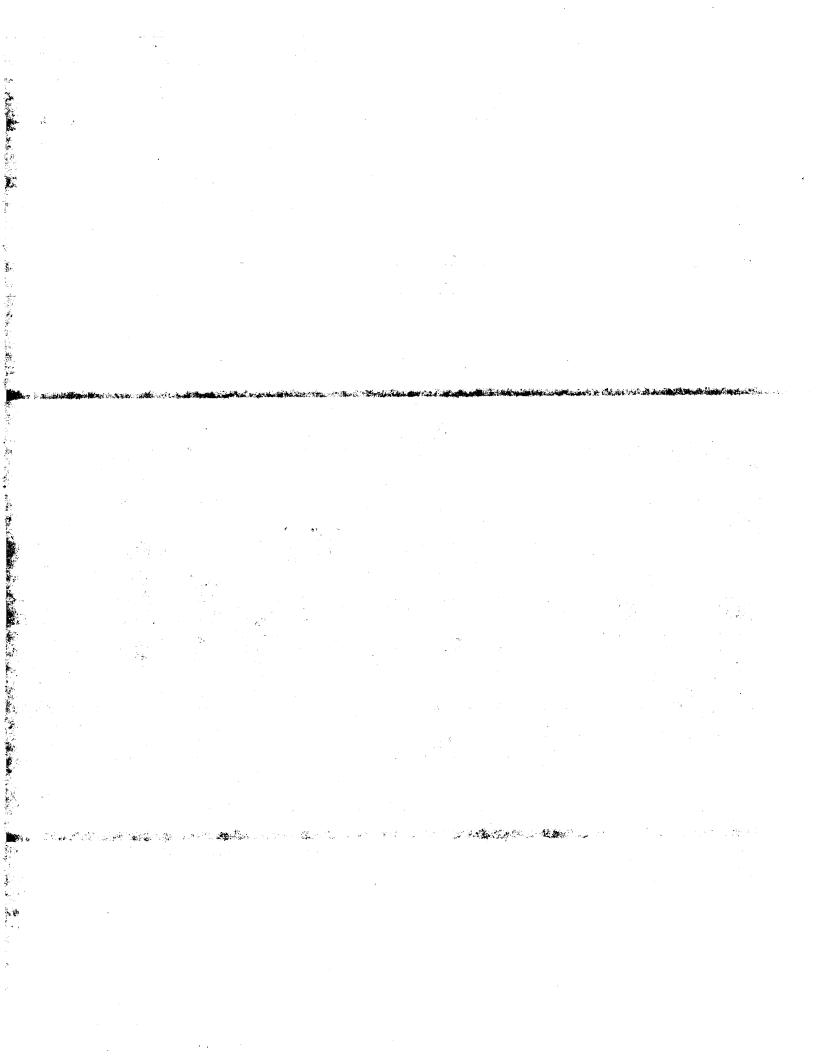
3: /cgn2_6/ptodata/3

4: /cgn2_6/ptodata/3

5: /cgn2_6/ptodata/3

6: /cgn2_6/ptodata/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      January 28, 2003, 10:38:10 ; Search time 54 Seconds (without alignments) 85.188 Million cell updates/sec
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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15
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                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 REFNSLPNNKASSDT 15
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                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                   IJ
                                                                                                                                                                          SUMMARIES
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                                                                                Description
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Search completed: January 28, 2003, 13:19:48 Job time: 54 secs

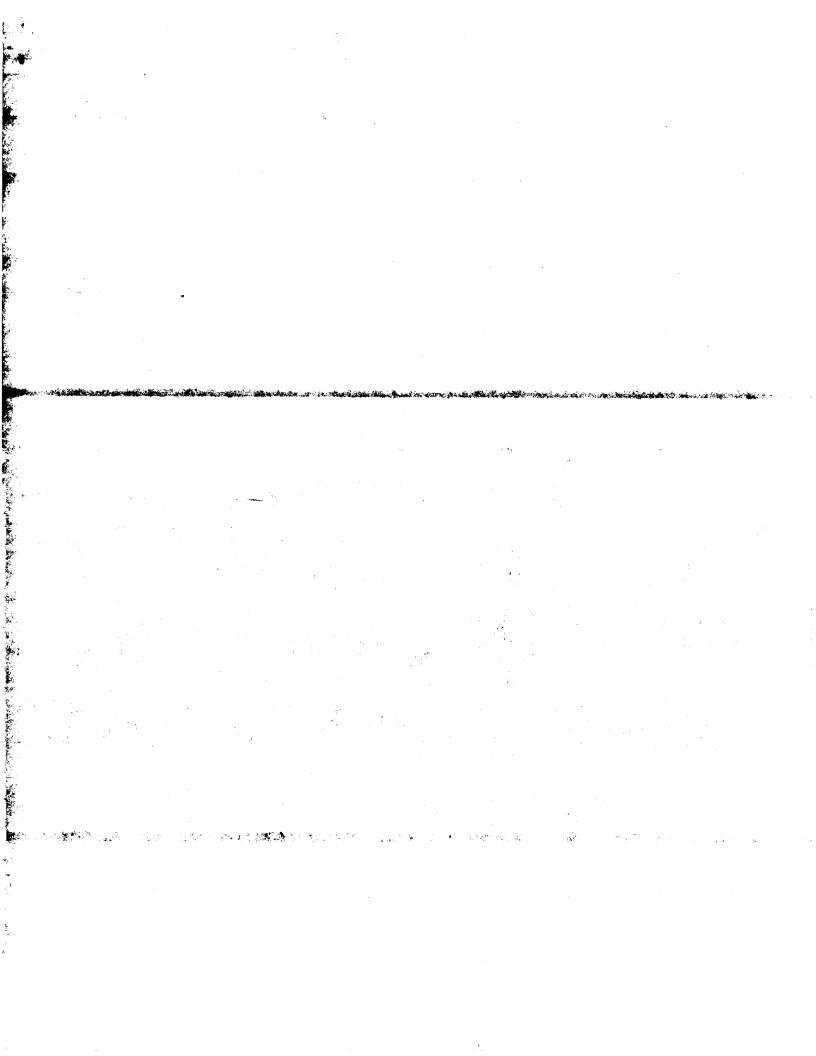


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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -Qe/Ggn2_1/USPTQ_Spool/BORIN682/runat_23012003_130142_7908/app_query.fasta_1.597
-OBS-Published_Applications_NA -QFMT=fastap_SUFFIX=0.1ip2n .rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=0-ligo
-TRANS-human40.cdi -LIST=1000 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=8
-ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-BORIM682_CGN 1_1_33_@TUNAT_23012003_130142_7908
-NCGU=6 -LCGU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Perfect score:
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-MODEL-frame+_p2n.model -DEV-xlh
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Maximum DB seq
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                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
                                                                                                                                                                                                                                                  Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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length: 2000000000
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Ygapop 60.0 , X
Fgapop 6.0 , E
Delop 6.0 , F
Query
Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396772 seqs,
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Ygapext 60.0
Fgapext 7.0
Delext 7.0
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                                                                                         SUMMARIES
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Description
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No matches found

Search completed: January 28, 2003, 13:23:11 Job time: 63 secs



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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLIGO Gapop 60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908470 segs, 133250620 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                     A_Geneseq_101002:*
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SUMMARIES
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Result No.	Score	Query	Query Match Length DB	DB	ID	Description
μ	15	100.0	237	23	ABB07780	E coli mutant heat
N	15	100.0	240	19	AAW65074	E. col
ω	15	100.0	240	23	ABB07778	E coli
4	15	100.0	258	σ	AAP50190	Sequence encoded b
Մ	15	100.0	258	σ	AAP50191	Sequence encoded b
σ	15	100.0	259	21	AAY96646	Plant-
7	15	100.0	259	21	AAY96647	Synthetic E. coli
89	15	100.0	259	21	AAY96648	Plant-
Q	15	100.0	259	21	AAY96650	Plant-optimized E
10	15	100.0	370	Š	ABB07785	

Query Match

100.0%; Score 15;

DB 23; Length 237;

SQ		X P.	X P I	Y R	PA PA	Y PR	X P	X P I	XX	N X	XXXX	X D	X Di	X AC	RES ABB ID XX		
Sequence	The str del com have culcultox	Claim	Pre	WPI;	(DOKU- (HGET (FUJI-	07-AUG	07-AUG	19-ғев-	JP2	Escherichia	LT; vacc	E coli	17-JUN-	ABB07780	RESULT 1 ABB07780 ID ABB077		111 112 113 114 115 116 116 117 118 119 119 119 119 119 119 119 119 119
ЭЭС		6; F	paration	2002-:	000	3-2000;	3-2000;	3-2002	002051779-	cichi	heat-la ine; mu	mutant	1-2002	780;	80 s		155 155 155 150 100 100 100 100 100 100
237 AA;	ucture of 1A5B in wetter of 1A	Fig 3; 27pp;	of a	299402/34	DOKURITSU GYOS HIGETA SHOYU I FUJITA GAKUEN	0; 2000JP	0; 2000JP	2.	79-A.	a coli.	labile toxi mutant; mLT	ant heat-	2 (first		tandard;		100.0 66.7 66.7 66.7 66.7 66.7 66.7 66.7
	in which a in which in which in which in the out A method a method in Bround		protein	·	GYOSEI YU KK. UEN.	-023	-0238					labile	entry)		protein;		33 37 20 20 20 20 20 20 20 20 20 20 20 20 20
	a gen ch the it gen corder hod is re of Brevib ne by ne be u luence agment	Japane	having		ГОН	8740.	740.				cholera		Y)				220 220 20 20 20
	e encc DNA s e and of (F provi 1A5B 1 acillu sed in repres , used	še.	ing 1A5B structure		HOJIN NOGYO SEIBUTSU						toxin; CT;	toxin (mLT) A subunit			237 AA.	ALIGNMENTS	ABB07784 AAU00507 AAU00506 AAR44016 AAR44017 AAR44019 AAR44020 AAR44022 AAR44022 AAR44022 AAR44023 AAR44023 AAR44025
	oding a protein having a subunit sequence encoding each signal is the B subunit gene and they are a subunit gene) - (SD sequence gene)				J SH.						recombinant; adjuvant;	nit fragment.					E coli heat-labile E. coli heat-labil E. coli heat-labil "Lys-63" E.coli he "Lys-97" E.coli he "Tyr-97" E.coli he "Glu-107" E.coli h "Asp-104" E.coli h "Ser-104" E.coli h "Ser-106" E.coli h "Glu-114" E.coli h "Lys-114" E.coli h E.coli heat labile "Tyr-53" E.coli he "Tyr-53" E.coli he E.coli heat labil Peptide sequence f

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RESULT 2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 15; Conser
                                                                                                                               toxin subunit A (IT-A). This protein is used in a method resulting in a mutant LT-A protein which has the wild type Ala residue at position 72 changed to an Arg residue resulting in a toxin which retains its immunogenicity but is detoxified. Detoxification is defined in the specification as a reduction in toxicity relative to wild-type toxin, such that any residual toxicity is sufficiently low to allow use as an effective immunogenic composition in humans without significant side effects. The protein can be combined with an acceptable carrier in immunogenic compositions, optionally comprising an adjuvant and/or a second immunogenic antigen. Such compositions can be administered to prevent/treat disease in a subject e.g. traveller's diarrhoea in humans.
                                                                                  Sequence
                                                                                                                                                                                                                                       This sequence represents a fragment of an Escherichia coli heat labile toxin subunit A (LT-A). This protein is used in a method resulting in a
                                                                                                                                                                                                                                                                       Disclosure; Page -; 67pp; English.
                                                                                                                                                                                                                                                                                        Mutated Escherichia coli heat labile toxin subunit A - is immunogenic and detoxified relative to wild-type, useful e.g. in vaccines against E. coli enterotoxigenic strains and as an adjuvant
                                                                                                                                                                                                                                                                                                                                                       Giuliani MM,
                                                                                                                                                                                                                                                                                                                                                                                               31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09818928-A1
                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat labile toxin subunit A; LT-A; mutant; immunogen; detoxification; carrier; adjuvant; prevention; treatment; disease; diarrhoea; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli LT-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW65074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW65074 standard; protein; 240 AA
                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection;
   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                   Local
                     ш
                                                                                                        coli in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \vdash
                                                                                                             protein or compositions are especially administered as vaccines ful to prevent or treat infections by enterotoxigenic strain of
  SLRSAHLAGQSILSG
                     SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                    1998-272223/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLRSAHLAGQSILSG
                                         l Similarity
15; Conserv
                                                                                                       mammals
                                                                                   240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxic
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                      Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                               96GB-0022660
                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-IB01440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                      (especially humans)..
                                                  100.0%;
                     15
  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "partial sequence"
                                                                                                                                                                                                                                                                                                                                                     Rappuoli R;
                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                  Score 15; DB 19;
Pred. No. 6.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.2e-08;

Mismatches 0;
                                         Mismatches
                                         0;
                                                            Length 240;
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                                        0;
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                                      Gaps
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ACC XXX DT XXX
                                                                                                                                  RESULT 4
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                                                                                                                                                                                                                                                  AAP50190
         E.coli NCIB 11932
                                                 Sequence
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine.
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Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a gene encoding a protein having a subunit structure of 1A5B in which the DNA sequence encoding each signal is deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene)-(SD sequence gene)-(A subunit gene). A method is provided for the preparation of a protein having a subunit structure of 1A5B in which the above DNA is connected a vector expressible in Brevibacillus chosinensis and Brevibacillus chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli heat-labile toxin (LT) A subunit fragment, used for constructing a protein with the subunistructure of 1A5B.
Pig scours vaccine;
                                                                                         30-OCT-1991
                                                                                                                                     AAP50190;
                                                                                                                                                                              AAP50190 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Fig 1; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparation of a protein having 1A5B structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-299402/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DOKU-) DOKURITSU GYOSEI HOJIN
(HGET ) HIGETA SHOYU KK.
(FUJI-) FUJITA GAKUEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2000; 2000JP-0238740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2000; 2000JP-0238740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB07778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB07778 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT; heat-labile toxin; cholera toxin; CT; recombinant; adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                    1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                           SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heat-labile
                                         encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 AA;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                     (first entry)
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toxin; diarrhoea
                                         the pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry;
                                                                                                                                                                                                                                                                                                                                                                                                    100
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                                         scours heat labile toxin
                                                                                                                                                                              258 AA
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                                                                                                                                                                                                                                                                                                                                                                             Score 15; DE Pred. No. 6.2); Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 240;
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                                         (LT) LTA gene
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New toxoid as inactivated form of toxin obtd. from organism transformed by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1984;
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New toxoid as inactivated form of toxin for use in vaccines
                                                                                                                                                                                          12-DEC-1983;
                                                                                                                                                                                                                                 12-DEC-1984;
                                                                                                                                                                                                                                                                           19-JUN-1985
                                                                                                                                                                                                                                                                                                                    EP145486-A
                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP50191 standard; Protein; 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scours
                                           1985-148358/25.
DB; AAN50206.
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                                                                                                                                                 ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
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                                                                                                                                                                                                                                                                                                                                                                                                                                             11932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                          GW.
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Pred. No.
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6.6e-08;
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Matches
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                AAN50205 is the gene sequence of the natural LTA gene. The LTA gene the site directed mutant SDM1 (see AAN50206) is inactive. The inventors claim a vaccine prepn. active against plg scours which contains an inactivated LTA component, together with additional K88 antigens opt. with whole cells comprising the antigens or contg. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat-labile toxin; LT-A; adjuvant; anti-bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY96646 standard;
                                                                                                                                                        Example
                                                                                                                                                                                                    elicit immune responses in animals
                                                                                                                                                                                                                      New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic composition
                                                                                                                                                                                                                                                                                                                                                                                                   (BOYC-) BOYCE THOMPSON (MASO/) MASON H S. (ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                                                                                                                                                                                                                                                                                                                                            Mason HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200037609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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15; Conser
                                                                                                                                                        ۲.
                                                                                                                                                                                                                                                                                           AAA51106
                                                                                                                                                        Fig 1; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                            Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0113507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- signal_peptide
19..259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coli heat labile toxin A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLANT RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15; DE
Pred. No. 6.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transgenic plant; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.6e-08;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 258
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                                                                                                                                                                                                                        compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oral;
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RESULT 7
AAY96647
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
This is mutant S63K Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The wild-type serine was replaced with lysine at residue 63 of
                                                                                                                                                                                          (BOYC-)
                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat-labile toxin; LT-A; i
adjuvant; anti-bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY96647 standard; Protein; 259 AA.
                                        Example 2;
                                                           New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                 N-PSDB;
                                                                                                                                                      Mason
                                                                                                                                                                                                                             22-DEC-1998;
                                                                                                                                                                                                                                                     22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96647;
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                                                                                                                                                                             (ARNT/)
                                                                                                                                                                                                                                                                                                       WO200037609-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                2000-442653/38.
DB; AAA51147.
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                                                                                                                                                    , SH
                                                                                                                                                                          BOYCE THOMPSON INST PLANT RES. MASON H S. ARNTZEN C J.
                                      Page -; 103pp; English.
                                                                                                                                                    Arntzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli LT-A K63 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                             98US-0113507
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                                                                                                                                                                                                                                                                                                                                                    /label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                             /label= signal_peptide
/note= "20"
20...259
                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           'label= S63K
                                                                                                                                                    CJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT-A; LT-B; mutein; transgenic plant; vaccine; oral; terial; S63K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                           "Wild-type serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
6.7e-08;
                                                                                                                                                                                                                                                                                                                             is replaced by lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LTB subunit (LT-B) or a CTB subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce adible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the mature protein, which was caused by a codon change of TCC to AAG in the coding sequence. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accommodate the creation of a Nool restriction site around the initiator methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also
                      WPI; 2000-442653/38.
N-PSDB; AAA51544.
                                                              Mason HS,
                                                                                                                                                                   22-DEC-1999;
                                                                                                                                                                                             29-JUN-2000.
                                                                                                                                                                                                                      WO200037609-A2
                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                        кеу
                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                      Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; R192G.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant-optimized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96648 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NB:
                                                                                       (ARNT/)
                                                                                                    (BOYC-) BOYCE THOMPSON INST PLANT RES
                                                                                                                                           22-DEC-1998;
                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as adjuvants.
                                                                                      ARNTZEN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type sequence shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence does
                                                              Arntzen CJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                         98US-0113507
                                                                                                                                                                   99WO-US30747
                                                                                                                                                                                                                                                                                                                                                                                                                                            .
.
                                                                                                                                                                                                                                                                       /label= mature_protein
211
                                                                                                                                                                                                                                                                                              /label= signal_peptide 20..259
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                           /label= R192G
                                                                                                                                                                                                                                                                                                                                                                                                                                            coli LT-A G192 mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not appear in the specification, shown in AAY96647, which appears
                                                                                                                                                                                                                                             "Wild-type arginine is replaced by glycine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was made from Figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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New polynucleotides encoding LT-A or CT-A polypeptides for the

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RESULT 9
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible vaccines, especially oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is mutant R192G Escherichia coli heat-labile toxin (LT) A subunit (LT-A). The wild-type arginine was replaced with glycine at residue 192 of the mature protein, which was caused by a codon change of TCC to AAG in the coding sequence. The sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NcoI restriction site around the initiator methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant-optimized E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page -; 103pp; English.
                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial; A63K+R192G; double mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
22-DEC-1999;
                                                                                                         WO200037609-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia
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                                                29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence does not appear in the specification, it was made from wild type sequence shown in AAY96647, which appears in Figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLRSAHLAGQSILSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLI
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99WO-US30747
                                                                                                                                                                                                                                                                                                                                                     /label- mature_protein 82
                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                                                                                                         /label= signal_peptide
20..259
                                                                                                                                                                                                               /label- R192G
                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                            /label- S63K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coli LT-A A63K+R192G mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                         "the wild type arginine is replaced by glycine at position 192 of the mature sequence"
                                                                                                                                                                                                                                                                   "the wild type serine is replaced by lysine at position 63 of the mature sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB Z1;
Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Š 밁

19-FEB-2002.

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В
CC This is Escherichia coli heat-labile toxin (LT) A subunit (LT-A) double CC mutant $63K+R192G. The wild-type serine was replaced with lysine at cresidue 63 and wild-type arginine was replaced with glycine at codons and eliminates sequence motifs associated with spurious mRNA processing. A single codon insertion (GTG encoding valine) was made to accomodate the creation of a NcoI restriction site around the initiator CC methionine codon. Novel polynucleotides encode a mutant LT-A polypeptide cor a mutant vibrio cholerae cholera toxin (CT) A subunit (CT-A) cor CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotides compared to the comparises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the production of transgenic plants to produce edible corphylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.

CC Note: This sequence does not appear in the specification. It was constructed from the wild type LT-A shown in AAY96646 which is given to the constructed from the wild type LT-A shown in AAY96646 which is given to the constructed from the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions elicit immune responses in animals
                                                                                                                                                                                                                                          E coli mutant heat-labile toxin (mLT) 5B-SD-lA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mason HS, Arntzen CJ
                                                                                                                                                                                                                                                                         17-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                            ABB07785;
                                                                                                                                                                                                                                                                                                                                           ABB07785 standard; Protein; 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BOYC-) BOYCE THOMPSON INST PLANT RES.
(MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1998;
                              JP2002051779-A
                                                                            Peptide
                                                                                                         Peptide
                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                          LT; heat-labile toxin; cholera toxin; CT; recombinant; adjuvant; vaccine; mutant; mLT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page -; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                         SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0113507
                                                                          /note= "LT 5B subunit" 104..370
                                                                                                                            Location/Qualifiers
                                                              /note= "LT lA subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 11
ABB07784
ID ABB07
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                                                                                                                                                                                                                                                                                                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                     M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli mutant heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene)-(SD sequence gene)-(A subunit gene). A method is provided for the preparation of a protein having a subunit structure of 1A5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a gene encoding a protein having a structure of 1A5B in which the DNA sequence encoding each si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL40640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2000; 2000JP-0238740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2000;
WPI;
                   (DOKU-) DOKURITSU GYOSEI HOJIN (HGET ) HIGETA SHOYU KK. (FUJI-) FUJITA GAKUEN.
                                                                 07-AUG-2000; 2000JP-0238740
                                                                                         07-AUG-2000;
                                                                                                               19-FEB-2002
                                                                                                                                     JP2002051779-A
                                                                                                                                                                   Peptide
                                                                                                                                                                                                       Key
                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                     vaccine
                                                                                                                                                                                                                                                              LT; heat-labile toxin; cholera toxin; CT; recombinant; adjuvant;
                                                                                                                                                                                                                                                                                                            17-JUN-2002
                                                                                                                                                                                                                                                                                                                                 ABB07784;
                                                                                                                                                                                                                                                                                                                                                       ABB07784 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 9-10; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparation of a protein having 1A5B structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOKU-) DOKURITSU GYOSEI HOJIN (HGET ) HIGETA SHOYU KK. (FUJI-) FUJITA GAKUEN.
                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                   coli heat-labile toxin (LT) 5B-SD-1A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           1 SLRSAHLAGQSILSG
2002-299402/34
                                                                                                                                                                                                                                                                                                                                                                                                               SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-299402/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (mLT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5B-SD-1A protein.
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                       2000JP-0238740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-0238740
                                                                                                                                                          104..37
/note=
                                                                                                                                                                              /note= "LT 5B subunit"
                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                               .373
e= "LT lA subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                               212
                                                                                                                                                                                                                                                                                                                                                        373
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15;
Pred. No.
                                          NOGYO SEIBUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOGYO SEIBUTSU
                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    le-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                          HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signal is
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 12
AAU00507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deleted from the A subunit gene and the B subunit gene and they are combined tandemly in the order of (B subunit gene) (SD sequence gene). (A subunit gene). A method is provided for the preparation of a protein having a subunit structure of 1A5B in which the above DNA is connected to a vector expressible in Brevibacillus chosinensis and Brevibacillus chosinensis and Brevibacillus chosinensis is transformed by said vector and said transformant is cultured. The protein can be used in the preparation of an adjuvant for vaccine. The present sequence represents the E. coli heat-labile toxin
                                            Park EJ,
                                                                                         15-SEP-1999;
                                                                                                                15-SEP-1999;
                                                                                                                                                              WO200119998-A1
                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                      Misc_feature
                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                    Misc_feature
                                                                                                                                                                                                                                                                                           Misc_feature
                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                        Escherichia coli strain K88ac
                                                                                                                                                                                                                                                                                                                                                              Heat-labile enterotoxin; LT; LTS63Y; LTdell110/112; mutant; detoxified and immunologically active protein; ADP-ribosylation; Gs; endotoxin; diarrhoea; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                           E. coli heat-labile enterotoxin (LT) mutant LTdel110/112
                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU00507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU00507 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a gene encoding a protein having a subunit structure of 1A5B in which the DNA sequence encoding each signal is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABL40639
                                                                                                                                         22-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7-8; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5B-SD-1A protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
15; Conserv
                                                                   MOGAM BIOTECHNOLOGY
                                            Kim JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of a protein having 1A5B structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                         99WO-KR00555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                99WO-KR00555
                                                                                                                                                                                               /note=
257
                                                                                                                                                                                                                      /note=
58..72
/note=
61
                                                                                                                                                                                                                                                                       44
                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                               /note=
                                          Chang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                              "Important residue for
                                                                                                                                                                                    "Encoded by TG"
                                                                                                                                                                                                                                 "Forms the NAD-binding
                                                                                                                                                                                                                                                       "Important residue for
                                                                                                                                                                                                          "Important residue for enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0%;
                                                                  RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 AA
                                            Yum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                           Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
                                            S
                                                                                                                                                                                                                                  site
                                                                                                                                                                                                                                                                               enzymatic activity"
                                                                                                                                                                                                                                                        enzymatic activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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N-PSDB; AAS01506 WPI; 2001-281524/29

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RESULT 13
AAU00506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type LT. The substitution of Ser to Tyr at position 63 in LTS63Y blocks NAD-binding. Deletion of Glu residues at positions 110 and 112 in LTG61110/112 eliminate the enzymatic activity of LT. The Al subunit of wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that regulates cAMP levels. The resulting increase in cAMP is the cause of diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities of mutant heat-labile endotoxins LTS63Y and LTdell10/112 were tested. Groups of mice were immunised with LTS63Y or LTdell10/112. The control groups received phosphate buffered saline (PBS) alone. The serum and faecal antibody titres to LT were determined. The results showed that mice immunised with LTS63Y or LTdell10/112 contained high and compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 42-44; 48pp; English
WO200119998-A1
                                                                                                                                                                                                                                                                                                                                               Heat-labile enterotoxin; LT: LTS63Y; LTdell110/112; mutant; detoxified and immunologically active protein; ADP-ribosyl
                                                                                                                                                                                                                                                                                                                                                                                            E. coli heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents Escherichia coli heat-labile enterotoxin (LT) mutant LTdell10/112. LTS63Y (AAU00506) and LTdell10/112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as adjuvant
                                          Misc-difference
                                                                                                Misc_feature
                                                                                                                             Misc-difference
                                                                                                                                                                                                                 Misc_feature
                                                                                                                                                                                                                                              Misc_feature
                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU00506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU00506 standard; Protein; 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                        Misc_feature
                                                                                                                                                                                                                                                                                                       Escherichia coli strain K88ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLRSAHLAGQSILSG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel detoxified and immunologically active proteins (IT derived by site-directed mutagenesis of the Al subunit of wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                        /note-
259
                                                                      /note=
112
                                                                                                /note-
110
                                                                                                                             /note=
63
                                                                                                                                                         /note=
                                                                                                                                                                                   /note=
58..72
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                note-
                                                                                                                                                                                                                                                                                                                                                                                            enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97
                         "Encoded by
                                                    "Important residue
                                                                                "Important
                                                                                                              "Substitution
                                                                                                                                       "Important residue for enzymatic activity"
                                                                                                                                                                                                 "Important residue for enzymatic activity"
                                                                                                                                                                                                                            "Important residue for enzymatic activity"
                                                                                                                                                                       "Forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15;
Pred. No.
                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                          (LT) mutant LTS63Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                    NAD-binding
                                                                                   residue
                                                                                                              of wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9.4e-08; ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                    for enzymatic activity"
                                                                                 for enzymatic activity"
                                                                                                              type
                                                                                                                                                                      site"
                                                                                                                                                                                                                                                                                                                                                ADP-ribosylation; Gs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 380;
                                                                                                              Ser to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 14
AAR44016
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                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc are two novel detoxified and immunologically active proteins (LT contents) derived by site-directed mutagenesis of the Al subunit of wild crype LT. The substitution of Ser to Tyr at position 63 in LT563y blocks (CR h)-binding, Deletion of Glu residues at positions 110 and 112 in CR LTdel110/112 eliminate the enzymatic activity of LT. The Al subunit of wild type LT catalyses ADP-ribosylation of Gs, a GTP-binding protein that regulates cAMP levels. The resulting increase in cAMP is the cause of CR diarrhoea in humans and animals e.g. pigs. The mucosal immunogenicities (CR of mutant heat-labile endotoxins LT563y and LTdel110/112 were tested. CR oroups of mice were immunised with LT563y or LTdel110/112. The control CR groups received phosphate buffered saline (PBS) alone. The serum and CR faecal antibody titres to LT were determined. The results showed that CR mice immunised with LT563y or LTdel110/112 contained high and CR comparable level of anti-LT antibodies in sera and faecal extracts compared with those immunised with wild-type LT. The LT mutants are useful as a vaccine for preventing and treating diarrhoea and as an antibody credition.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents Escherichla coll heat-labile enterotoxin (LT) mutant LTS63Y. LTS63Y and LTdell110/112 (AAU00507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                      Escherichia coli
                                                                                                                                                                  enterotoxigenic bacteria;
                                                                                                                                                                                                                               08-DEC-1993
                                                                                                                                                                                                                                                             AAR44016;
                                                                                                                                                                                                                                                                                          AAR44016 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New detoxified mutants of Escherichia coli heat-labile enterotoxin useful as vaccine for preventing and treating diarrhoea, and as ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001
                                                         Misc-difference
                                                                                                                                   ADP-ribosyltransferase
                                                                                                                                                                                                "Lys-63" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for antibody production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOGA-) MOGAM BIOTECHNOLOGY RES INST
                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                    1 SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                       SLRSAHLAGQSILSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Page 39-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 AA;
                                                                                                                                                  site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-KR00555
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                                                         62
                                           /note=
                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                    15
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                                                                                                                                                                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing and treating diarrhoea, and as adjuvant
           "corresponds to position 63 in cholera toxin A subunit; wild-type Ser is substituted by Lys to reduce toxicity"
                                                                                                                                   activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0%;
                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                            236
                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yum J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                   immunogenic
sis; reduced
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                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4e-08;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                  detoxified LT-A;
toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 15
AAR44017
ID AAR44
XX AAR4
AC AAR4
XX O8-DJ
XX ente
KW ente
KW prot
KW prot
KW ADP
XX ADP
XX ESC!
XX EH Key
FT Mis
FT FT
XX WO
XX ST
XX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-227320/28.
N-PSDB; AAQ51317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-DEC-1991;
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        31-DEC-1991;
                                                         30-DEC-1992;
                                                                                                             08-JUL-1993
                                                                                                                                                                  W09313202-A
                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR44017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR44017 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA;
                                                                                                                                                                                                                                                                                                                                                                                  coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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        91IT-0MI3513
                                                            92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heat
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                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hol W,
                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    activity
                                                                                                                                                                                                                "corresponds to position 97 in cholera toxin A subunit; wild-type Val is substituted by Lys to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10; DB 14; Pred. No. 0.0091; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĭ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 16
AAR44018
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigence E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 2 and Page 46; 60pp; English.
N-PSDB; AAQ51319
          WPI; 1993-227320/28
                                                                                                    30-DEC-1992;
                                                                                                                           08-JUL-1993.
                                                                                                                                                 WO9313202-A.
                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                          Escherichia
                                                                                                                                                                                                                                                               protomer A; site-direct
ADP-ribosyltransferase
                                                                                                                                                                                                                                                                          enterotoxigenic bacteria;
protomer A; site-directed
                                                                                                                                                                                                                                                                                                                                   08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                               AAR44018 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid numbering is based on the cholera toxin A subunit sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-227320/28.
N-PSDB; AAQ51318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domenighini M,
                                Domenighini M,
                                                        (BIOC-)
                                                                              31-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                          AAR44018
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SLRSAHLAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conserv
                                                        BIOCINE
                                                                                                                                                                                                                                                                                                            E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA;
                                                                                                                                                                                                                                           coli
                                                                                                                                                                                                                                                                         site-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                              91IT-0MI3513
                                                                                                    92WO-EP03016
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                                 Hol
                                                        SCLAVO SPA.
                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                            heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCLAVO
                                                                                                                                                                                            /note=
                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPA.
                                                                                                                                                                       "corresponds to position 97 in cholera to
A subunit; wild-type Val is substituted
Tyr to reduce toxicity"
                                                                                                                                                                                                                                                                activity.
                                 Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .08;
                                                                                                                                                                                                                                                                          mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                 236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rappuoli
                                Rappuoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
0.0091;
                                 ₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                           toxicity;
                                                                                                                                                                                                                                                                                       detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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AAR44019
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enterotoxin producing Escherichia coli
                                 Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                      Ney Location/Qualifiers Misc-difference 103
                                                                                                                                                                                                                                                                                                                                                                                   enterotoxigenic bacteria; vaccine; immunogenic
protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
           Claim
                                                                                                                                                                                                                       08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR44019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR44019 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                               WPI; 1993-227320/28
                                                                                                                       Domenighini M,
                                                                                                                                                                        31-DEC-1991;
                                                                                                                                                                                              30-DEC-1992;
                                                                                                                                                                                                                                               W09313202-A
                                                                                                                                                                                                                                                                                                                                                                        ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                        "Glu-107"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLRSAHLAGQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      numbering is based on the cholera toxin A subunit sequence)
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                                                                                  AAQ51320
                                                                                                                                               BIOCINE
         Fig
                                                                                                                                                                                                                                                                                                                                                                                                                        E.coli heat labile toxin subunit A.
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                                                                                                                                                                                              92WO-EP03016
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                                                                                                                                               SCLAVO SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                    "corresponds to position 107
A subunit; wild-type His is
Glu to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                        activity.
           46;
                                                                                                                       Pizza
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          60pp; English
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Pred. No. 0.0
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0.0091;
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toxicity;
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RESULT 18
AAR44020
ID AAR44
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XX AAR44
XX OB-DE
DE "Lys-
XX Ente
DY OB-DE
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Best Local
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The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al., J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enterotoxigenic bacteria; vaccine; imm
protomer A; site-directed mutagenesis;
                                                                                                                                                                                                                                                                                      Immunogenic detoxified mutant cholera toxin and heat labile to useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                   enterotoxin
                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Domenighini M,
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DB; AAQ51321.
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                                                                                                                                                                                                               3; Fig
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                                                                                                                                                                                                               2 and Page 46;
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                                                                                                                                                                                                            English.
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sis; reduced
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0.0091;
hes 0;
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toxicity;
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RESULT 19
AAR44021
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XX AAR4
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Best Local S
Matches 10
                                                                        The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamotto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic detoxified mutant cholera toxin and heat labile toxin - useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                    numbering is based
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DB; AAQ51322.
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                                                                                                                                                                                                                                                                                                                                                                               Fig 2 and Page 46; 60pp; English.
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "corresponds to position 104
A subunit; wild-type Tyr is
Asp to reduce toxicity"
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                                                       on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pizza
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Pred. No.
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red. No. 0.0091;
Mismatches 0
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                                                    toxin A subunit sequence).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in cholera toxin substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                   ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Db Qy

64

SLRSAHLAGQ

1 SLRSAHLAGO

10

Matches

10;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0;

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RESULT 20
AAR44022
                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
                                                         protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamannoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxigenic bacteria; protomer A; site-directed ADP-ribosyltransferase act
                                    Sequence
                                                                                                                                                                                                     Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                               enterotoxin
                                                                                                                                                                                                                                          Immunogenic - useful as
                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                         WPI; 1993-227320/28.
                                                                                                                                                                                                                                                                                                             Domenighini M,
                                                                                                                                                                                                                                                                                                                                      (BIOC-) BIOCINE SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                     W09313202-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR44022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR44022 standard;
                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SLRSAHLAGQ 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRSAHLAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                              AAQ51323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.coli heat
                                     236
                                                                                                                                                                                                                                         detoxified mutant cholera toxin and heat labile toxin vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                              producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                     AΑ;
                                                                                                                                                                                                                                                                                                                                                              91IT-0MI3513
                                                                                                                                                                                                                                                                                                                                                                                     92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                Hol W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
66.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
100.0%;
                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :, vaccine; immunogenic
ted mutagenesis; reduced
activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      labile
                                                                                                                                                                                                                                                                                                                                       SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "corresponds to position 104 A subunit; wild-type Tyr is Ser to reduce toxicity"
                                                                                                                                                                                                                                                                                                                Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
 Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                               coli
                                                                                                                                                                                                                                                                                                               Rappuoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit
 DB 14;
0.0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14;
0.0091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detoxified LT-A;
           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in cholera substituted
            236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT 22
AAR44024
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AAR44023
ID AAR44
                                                                                                                                                                                                                                                                                                             AX U
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                                                                                                                                            밁
                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                            The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence and the description given in the text. (N.B. Amino acid sequence acid 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity.
                                    AAR44024 standard; Protein; 236
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterotoxin producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09313202-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR44023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR44023 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOC-) BIOCINE SCLAVO SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Ser-106"
                                                                                                                                            64
                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                  numbering
                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                             236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         col1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .coli
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                      is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91IT-0MI3513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hol W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heat
                                                                                                                                                                                                                                                                                                                                                      based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                              66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "corresponds to position 106 A subunit; wild-type Pro is Ser to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                    on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pizza
                                                                                                                                                                                                                                                                                                                                               the cholera toxin A subunit sequence)
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĭ
                                       A
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rappuoli
                                                                                                                                                                                                                        DB 14; I
0.0091;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detoxified LT-A;
toxicity;
                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in cholera toxin substituted by
                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                        Gaps
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RESULT 23
AAR44025
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                                                                                                                    H
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                            The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates to immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
enterotoxigenic bacteria; vaccine; immu
protomer A; site-directed mutagenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers Misc-difference 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                 08-DEC-1993
                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                           AAR44025;
                                                                                                                  AAR44025 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-1993
                                      "Lys-114" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1992;
                                                                                                                                                                                    64
                                                                                                                                                                                                1 SLRSAHLAGQ
                                                                                                                                                                                    SLRSAHLAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1993-227320/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ51325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                         236
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                (first entry)
                                                                                                                                                                                                                                                                                         AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91IT-0MI3513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-EP03016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOl W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCLAVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                    Protein;
                                                                                                                                                                                                                                                  66.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "corresponds to position 114 in cholera toxin A subunit; wild-type Ser is substituted by Glu to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pizza
vaccine; immunogenic
mutagenesis; reduced
                                                                                                                                                                                                                                  Score 10; DB; Pred. No. 0.0 0; Mismatches
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rappuoli R;
                                                                                                                                                                                                                                                  DB 14;
0.0091;
                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detoxified LT-A;
toxicity;
toxicity;
            detoxified
                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                     Gaps
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ADP-ribosyltransferase

activity

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RESULT 24
AAR38728
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                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                   The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J. Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutatin is not printed in the specification but has been assembled from the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 2 and Page 46; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ney
Location/Qualifiers
Misc-difference 110
08-JUL-1993
                        WO9313202-A
                                                                       protomer A; site-directed mutagenesis;
ADP-ribosyltransferase activity.
                                                                                                 enterotoxigenic bacteria; vaccine;
                                                                                                                       E.coli heat labile toxin subunit A
                                                                                                                                                   08-DEC-1993
                                                                                                                                                                                                   AAR38728 standard;
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterotoxin producing Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9313202-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOC-) BIOCINE SCLAVO SPA.
                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                               1 SLRSAHLAGQ 10
||||||||||
64 SLRSAHLAGQ 73
                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1993-227320/28.
                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ51326
                                                                                                                                                                                                                                                                                                                                                                  236 AA;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91IT-0MI3513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                    Protein; 236
                                                                                                                                                                                                                                                                                                                            66.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "corresponds to position 114 A subunit; wild-type Ser is Lys to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pizza
                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
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                                                                                                                                                                                                    A
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                                                                                   immunogenic detoxifie
sis; reduced toxicity;
                                                                                                                                                                                                                                                                                                                            DB 14;
0.0091;
                                                                                                 detoxified LT-A;
                                                                                                                                                                                                                                                                                                                                       Length 236,
                                                                                                                                                                                                                                                                                                                 Indels
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substituted
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RESULT 25
AAR38730
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Best Local
                                                                                                                                                                                                                                                enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced ADP-ribosyltransferase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the sequence of the A subunit of the heat labile toxin (LT-A) of a Strain of E.coli known to affect humans. The sequence was published by Yamamoto et al, J.Biol. Chem., 259, 5037-5044.

Mutations at selected positions within this sequence have been found to reduce toxicity (see AAR38730-R38732 and AR84016-R44025). The invention relates to such immunogenic detoxified proteins and their use in vaccines to protect against enterotoxigenic E.coli.
WPI; 1993-227320/28.
N-PSDB; AAQ51314.
                                                                                                                    08-JUL-1993.
                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domenighini M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOC-) BIOCINE SCLAVO SPA.
                               Domenighini M,
                                                     (BIOC-)
                                                                         31-DEC-1991;
                                                                                               30-DEC-1992;
                                                                                                                                          WO9313202-A.
                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                           "Asp-53" E.coli heat labile toxin subunit A.
                                                                                                                                                                                                                                                                                                                 08-DEC-1993
                                                                                                                                                                                                                                                                                                                                      AAR38730
                                                                                                                                                                                                                                                                                                                                                          AAR38730 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                                                                                                              SLRSAHLAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
10; Conserv
                                                     BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 AA;
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                                                                                                                                                                                                                                                                                                                (first entry)
                                                                         91IT-0MI3513
                                                                                                92WO-EP03016
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                                Hol
                                                     SCLAVO SPA.
                                                                                                                                                                                             Location/Qualifiers 52
                                                                                                                                                                                                                                                                                                                                                                                                              73
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                                                                                                                                                                                   /note=
                                Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
100.0%;
                                                                                                                                                            "corresponds to position 53 in cholera to
A subunit; wild-type Val is substituted
Asp to reduce toxicity"
                                Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No.
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                               Rappuoli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
0.0091;
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                                                                                                                                                                                                                                                                       detoxified LT-A;
                                                                                                                                                                                                                                                             toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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RESULT :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
            Claim
                                           Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and
                                                                                                                                                                                                                                                                                                                                                                              enterotoxigenic bacteria; vaccine; immunogenic protomer A; site-directed mutagenesis; reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                  enterotoxin
                                                                                  N-PSDB;
                                                                                                                     Domenighini M,
                                                                                                                                                                                              30-DEC-1992;
                                                                                                                                                                                                                      08-JUL-1993.
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                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                   ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                    "Glu-53" E.coli heat labile
                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1993
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                                                                                                                                              BIOCINE
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                                                                                  AAQ51315
           Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA;
                                                                                                                                                                                                                                                                                                                                            coli
                                  producing
                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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            2 and
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                                                                                                                                             SCLAVO SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
           Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
100.0%;
                                   Escherichia
                                                                                                                                                                                                                                                                  "corresponds to position 53 in cholera A subunit; wild-type Val is substitute Glu to reduce toxicity"
                                                                                                                                                                                                                                                                                                                                                                   activity.
          46; 60pp; English
                                                                                                                      Pizza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236
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                                                                                                                                                                                                                                                                                                                                                                                                                    toxin subunit A.
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Pred. No.
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                                   COLI
                                                                                                                    Rappuoli
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0.0091;
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                                                                                                                                                                                                                                                                                                                                                                              detoxified LT-A;
toxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                               substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                           toxin
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RESULT 27
AAR38732
ID AAR38
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al, J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of this preferred detoxified mutein is not printed in the sequence and the description given in the full-length wild-type sequence and the description given in the text. (N.B. Amino acid numbering is based on the cholera toxin A subunit sequence).
The wild-type sequence coding for the A subunit of the heat labile toxin (LT-A) of a strain of E.coli known to affect humans (Yamamoto et al., J.Biol. Chem., 259, 5037-5044 - see AAQ42768) was subjected to site-directed mutagenesis. Certain mutations were found to reduce toxicity (see AAR38730-32 and AAR44016-R44025). The invention relates immunogenic, detoxified LT-A proteins and their use in vaccines to protect against enterotoxigenic E.coli. The amino acid sequence of
                                                                                                                                 Immunogenic detoxified mutant cholera toxin and heat labile toxin useful as vaccines against infection by Vibrio cholerae and enterotoxin producing Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enterotoxigenic bacteria; vaccine; immunogenic
protomer A; site-directed mutagenesis; reduced
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                                                                                                          Claim
                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                       WPI; 1993-227320/28
                                                                                                                                                                                                                                                                                                                                             08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
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                                                                                                                                                                                                                                  Domenighini M,
                                                                                                                                                                                                                                                           (BIOC-)
                                                                                                                                                                                                                                                                                                                  30-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP-ribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Tyr-53" E.coli heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLRSAHLAGQ
                                                                                                         3; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                         2 and Page
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                                                                                                                                                                                                                                                             SCLAVO
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  labile
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                                                                                                                                                                                                                                                              SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity.
                                                                                                          46;
                                                                                                                                                                                                                                   Pizza
                                                                                                       60pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin subunit A.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detoxified LT-A;
toxicity;
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Best Local
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                                                                                                                         This sequence corresponds to the amino acid sequence of the A subunit of the E. coli heat labile toxin, an example of a bacterial ADP-ribosylating toxin. A mutant detoxified form of this protein is used in a parenteral adjuvant composition, which comprises the detoxified protein, at least one selected antigen and optionally a pharmaceutically acceptable (optionally topical) vehicle. The adjuvant composition can be administered parenterally in conjunction with at least one antigen in methods to immunise vertebrate subjects. The adjuvant has the ability to enhance the humoral and cell mediated immune responses elicited by the antigen (e.g. by making the antigen more strongly immunogenic or necessitating fewer/lower antigen doses). It can be administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A subunit; heat labile toxin; ADP-ribosylation; mutant; detoxification; parenteral adjuvant; antigen; immunisation; humoral response; cell-mediated immune response; virus; bacterium; parasite; fungus; tumour; allergen; pathogen; AIDS; autoimmune disease; cancer; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       this preferred detoxified mutein is not printed specification but has been assembled from the \ensuremath{\mathrm{fu}}
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                       prior/subsequent to the antigen, and is preferably administered within a short space of time to the same site; it can also be administered in isolation from antigens as a boost following systemic or mucosal antigen administration. Most preferably, the adjuvant is co-administered with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detoxified mutants of bacterial ADP-ribosylating toxins as parenteral adjuvants - useful to enhance humoral and cell-mediated immune responses in vertebrates when administered with selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1A-B; 51pp; English
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21-MAR-1997;
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DB; AAV81595.
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10; Conserv
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in the compositions and a pharmaceutically
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97US-0041227
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease; diagnosis
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5. 0.0091;
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RESULT 29
AAU14105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carrier. The antigen may be derived from viruses, bacteria, paras and fungi or may be tumour antigens, self-antigens and allergens. compositions are therefore useful in the treatment and prevention e.g. viral diseases, allergic manifestations, diseases caused by pathogens (e.g. bacteria or parasites), AIDS, autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g. Systemic Lupus Erythematosus), Alzheimer's disease and cancers The adjuvant can also be used to prepare antibodies against selected antigen(s), useful e.g. for diagnostic purposes or for antigen
                                                                                                                                                                                                                                                                                                                              Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antivior intracellular modulatory activity, by detecting the formation of DP107/DP178 complex -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-retroviral; DP178-like; DP107-like; heat labile antifusogenic; antiviral; HIV transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide sequence from Escherichia coli heat labile enterotoxin A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TRIM-) TRIMERIS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1999;
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Pred. No.
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0.0092;
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present sequence represents a peptide sequence

from Escherichia

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CC heat labile enterotoxin A.

XX

Sequence 234 AA:

OBST MARCH

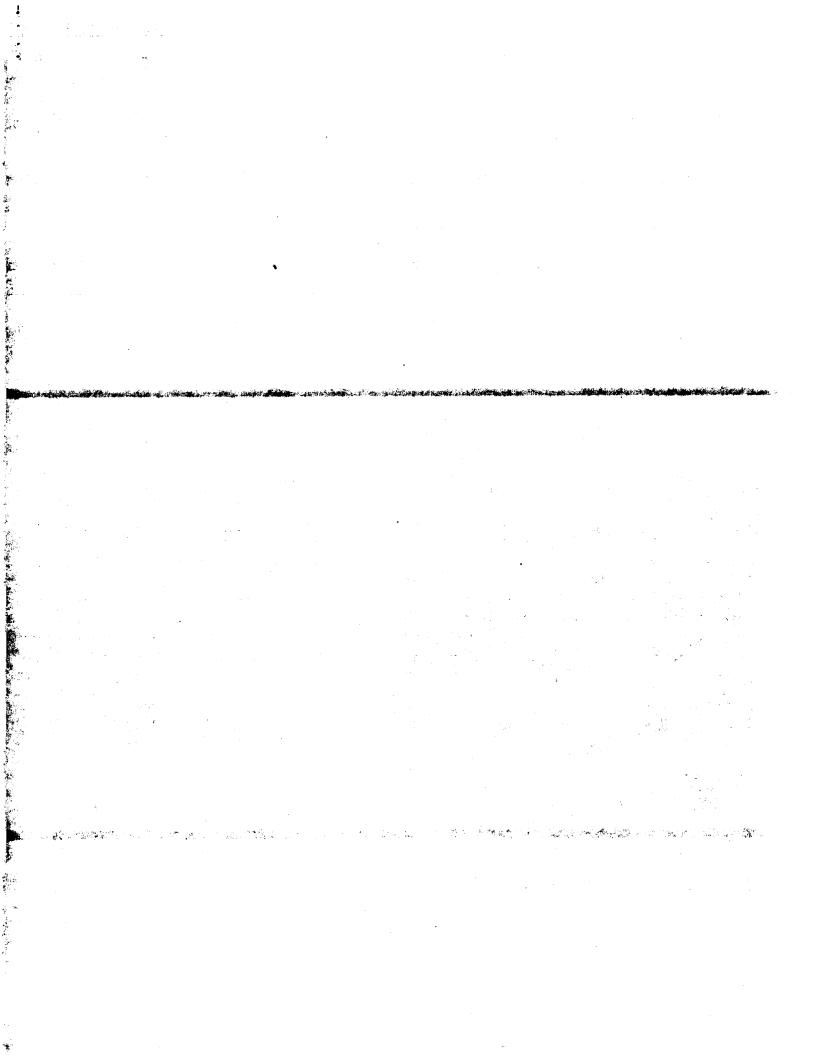
Dept Local Similarity 100.04, Prod. No. 0.0097, Indels 0; Gaps 0;

NRICHES 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12.USANIAGQ 10

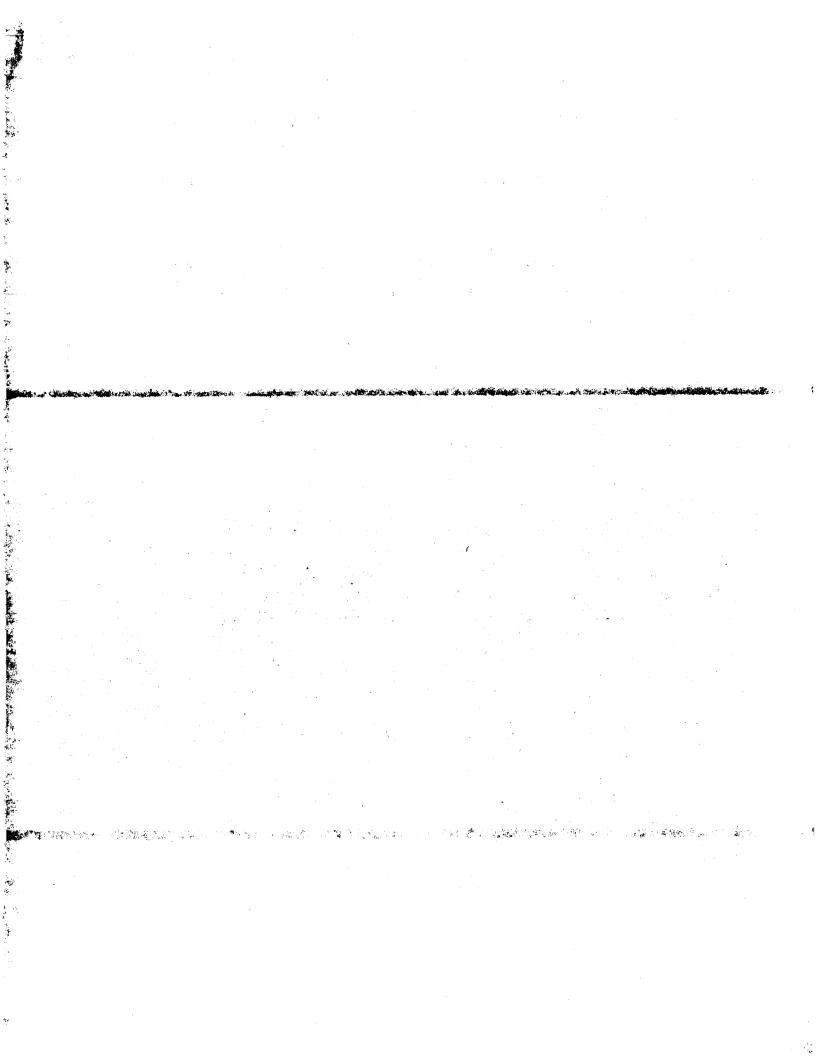
Search completed: January 28, 2003, 10:32:17

Job time: 127 secs
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A;Cross references: GB:R01995; NID:g148027; PIDN:AAA24685.1; PID:g148028
R;Spicer, E.K.; Noble, J.A.
J. Biol. Chem. 257, 5716-5721, 1982
A;Title: Escherichia coli heat-labile enterotoxin. Nucleotide sequence of the A subunit A;Reference number: A01817; MUID:82167425; PMID:6279611
A;Accession: A01817
A;Molecule type: DNA
A;Residues: 1-21, 'R', 23-36, 'FRS', 40-44,46-92, 'Y', 94-99, 'LTIYI', 105-107,111-118, 'IS', 121-A;Cross-references: EMBL:V00275; NID:g41339; PIDN:CAA23532.1; PID:g41340
                                                                                                                                                                                                                                                                                                  C;Species: Escherichia coli
C;Date: 30-Apr-1991 #sequence_revision 17-Oct-1997 #text_change 18-Jun-1999
C;Accession: I55231; A01817; A26946
R;Yamamoto, T.; Tamura, T.; Yokota, T.
J. Biol. Chem. 259, 5037-5044, 1984
A;Title: Primary structure of heat-labile enterotoxin produced by Escherichia coli patho
A;Reference number: I55231; MUID:84185610; PMID:8325417
A;Accession: I55231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Result
No.
                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-258 < RES>
                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat-labile enterotoxin A precursor - Escherichia C; Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Score Match Length DB
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pir3:*
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(without alignments)
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A;Gene: eltA
C;Superfamily: heat-labile enterotoxin chain A
C;Keywords: enterotoxin
E;1-18/Domain: signal sequence #status predicted <SIG>
F;19-258/Product: heat-labile enterotoxin chain A #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: the authors translated the codon TAT for residue R;Yamamoto, T.; Gojobori, T.; Yokota, T. J. Bacteriol. 169, 1352-1357, 1987.
A;Title: Evolutionary origin of pathogenic determinants 1 A;Reference number: A26946; MUID:87137303; PMID:3546273 A;Accession: A26946
                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-21, 'R',23-206, 'N',208-230,'E',232-255,'D',257-258 <YAM> A;Cross-references: EMBL:M15363 C;Comment: The heat-labile enterotoxin molecule contains one A chain and five or
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C;Genetics:
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                                                                                      STRAIN-078:H11 / H10407;
MEDLINE-84185610; PubMed-6325417;
Yamamoto T., Tamura T., Yokota T.;
"Primary structure of heart-labile enterotoxin coli pathogenic for humans.";
J. Biol. Chem. 259:5037-5044(1984).
                                                                                                                                                                                                                                                                                                P43530;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heat-labile enterotoxin A chain precursor (LT-A,
                    REVISION TO 207.
STRAIN=078:H11 / H10407;
MEDLINE=87137303; PubMed=3546273;
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Bacteria; Proteobacteria; gamma
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STRAIN-Isolate PCG86, and Isolate P307;
MEDLINE-87137303; PubMed-3546273;
                                                                                                       Bacteria; Proteobacteria; Escherichia.
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-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
                                                                                                                                                 Escherichia coli
                                                                                                                                                                     ELTA OR LTPA.
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EMBL; S60731; AAC60440.1;
HSSP; P06717; 1LTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Bacteriol. 169:1352-1357(1987).
                                                                                                                                                                                   Heat-labile enterotoxin
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Pfam; PF01375; Enterotoxin_A;
PRINTS; PR00771; ENTEROTOXINA.
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SIGNAL 1
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MEDLINE=93252225; PubMed=8480
Inoue T., Tsuji T., Koto M.,
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Amino acid sequence of heat-labile enterotoxin from c
anterotoxigenic Escherichia coli is identical to that
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Gojobori T.,

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STRAIN-ISOlate P307;
Dykes C.W., Halliday I.J., Hobden A.N., Read
"A comparison of the nucleotide sequence of
labile enterotoxin and cholera toxin.";
labile enterotoxin and cholera toxin.";
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J. Bacteriol. 169:1352-1357(1987).
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Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R
Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R
"Identification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins of Escherichia coli and Vibrio cholerae.";
Mol. Microbiol. 15:1165-1167(1995).
-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-i- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE=91238966; PubMed=2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Witholt B., Hol W.G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixma T.K., van Zanten B.A.M., Dau 
"Refined structure of Escherichia 
close relative of cholera toxin."; 
J. Mol. Biol. 230:890-918(1993).
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MEDLINE=82167425; Pu
                                                                                                                                                                                                                                                                                                                                                          Nature
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                        EMBL;
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J.D., Maas W.K.;
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                                                                                                                  license agreement (license@isb-sib.ch)
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S; PR00771; ENTEROTOXINA.
15; Conservative
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Search completed: January 28, 2003, 10:25:42 Job time: 12.6667 secs

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RESULT 1
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01-JUN-2001 (TREMBLrel. 17, Last annotation update)
Heat-labile enterotoxin A subunit.
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Search completed: January 28, 2003, 10:36:40 Job time: 53.3333 secs
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Vaccine 12:1083-1089(1994).

EMBL; AB011677; BAA25725.1; -.

EMSP; P06717; 1LTG.

InterPro; IPR001144; Enterotoxin_A.

InterPro; IPR001886; ER_target.

Pfam; PF01375; Enterotoxin_A; 1.

PRINTS; PR00771; ENTEROTOXINA,

PROSITE; PS00014; ER_TARGET; UNKNOWN_1.

SEQUENCE 258 AA; 29331 MW; 2BB15D2774
                                                                                                                                                                                                                                                                                                  "Escherichia coli heat-labile enterotoxin B subunits supplemented with a trace amount of the holotoxin as an adjuvant for nasal influenza
                                                                                                                                                                                                                                                                                                                                       MEDLINE-95091056; PubMed-7998417;
Tamura S., Asanuma H., Tomita T., Komase K.,
Hattori N., Watanabe K., Suzuki Y., Nagamine
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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; Sequence 3, Application US/08823120
Patent No. 6149919
; GENERAL INFORMATION:
APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic D
TITLE OF INVENTION: Cholera Toxin
TITLE OF INVENTION: Their Use for
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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Immunogenic Detoxified Mutants of Cholera Toxin and of the Toxin Lt, Their Inheir Use for the Preparation of Vaccines
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US-08-866-099-114

US-08-360-107A-124

US-08-484-223B-114

US-08-919-597-114

US-08-475-668A-114

US-08-485-551A-114

US-08-485-551A-114

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Best Local Similarity
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APPLICANT: Domenighini, Mario
APPLICANT: Domenighini, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Toolera Toxin and of the Toxin Lt, Their Preparation
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0319
TELECOMMUNICATION INFORMATION:
                                                          ZIP: 94608-9916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                            STREET: 4500 CITY: Emeryville CTATE: California
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APPLICATION NUMBER: US C
FILING DATE: 11-NOV-1994
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COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,120
FILING DATE:
                                                 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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CITY: Emeryville
STATE: California
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                                APPLICATION NUMBER:
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TELEPAX: (510 (655-3542
INFORMATION FOR SEQ ID NO: 6:
                                                                                  INFORMATION FOR SEQ ID NO: 114:
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TYPE: amino acid
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APPLICATION NUMBER: US 0
FILING DATE: 11-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                  TELEFAX: (212,
TELEFAX: 66141 PENNIE
                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/486,099 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 SLRSAHLAGQ 73
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REFERENCE/DOCKET NUMBER: 0315.001
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                 STRANDEDNESS
                                    TYPE:
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o. 6013263
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                               amino acid
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Langlois, Alphonse J.
VENTION: COMPOSITIONS FOR INHIBITION OF
VENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
VENTION: B VIRUS TRANSMISSION

COMPOSITION: B VIRUS TRANSMISSION
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unknown
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Pred. No.
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RESULT 4
US-08-360-107A-124
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; MOLECULE TYPE:
US-08-360-107A-124
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                                                                        Query Match
Best Local !
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                                                         Matches
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: Langidis, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, IN
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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CITY: New York
STATE: New Yor
 82
                                                                       Local
                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                           NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 20-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                            STRANDEDNESS
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SLRSAHLAGO 91
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Lambert, Dennis M.
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                                                         Conservative
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                                                                                                                                                 unknown
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100.0%; Pr
                                                   66.7%; 5c.
100.0%; Pro
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                                                                       Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                           7872-013
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Pred. No.
                                                         Mismatches
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                                                                     DB 3;
0.004;
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0.004;
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US-08-484-223B-114; Sequence 114, Application US/08484223B

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Best Local :
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GENERAL INFORMATI
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NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
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SEQUENCE CHARACTERISTICS:
SEQUENTH: 254 amino acids
TYPE: amino acid
                                                                                                                                                      APPLICANT:
APPLICANT:
                                APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Lendbert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
                                                                                                                                                                                                              APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TOPOLOGY: unknown
MOLECULE TYPE: protein
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APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
                    CORRESPONDENCE ADDRESS
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CORRESPONDENCE ADDRESS:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/484,223B FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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ZIP: 10036-2711
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1155 Avenue of the Americas
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Matthews, Thomas J.
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                                                                                                                                                                                          Wild, Carl T.
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Pennie & Edmonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114, Application US/08475668A
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/:
APPLICATION NUMBER: US 08/:
TTTING DATE: 06-UN-1995
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                           COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compditible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: COTUZZI, Laura A.
REGIZATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
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MEDIUM TYPE: Floppy disk
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                         COUNTRY:
ZIP: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: a
                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0%; Ines 10; Conservative 0;
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Lambert, Dennis M.
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US-08-485-551A-114
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Best Local S
Matches 10
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APPLICANT: E
APPLICANT: W
APPLICANT: W
APPLICANT: E
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                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                             OPERATING CONTROL OF THE PROPERTY APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/08/485,551A
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 7877
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741/8864
             TOPOLOGY: un MOLECULE TYPE:
                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonses J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                              NAME: COruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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                                           STRANDEDNESS
                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
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                                                                           LENGTH:
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1155 Avenue of the Americas
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Lambert, Dennis M.
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                                                                                                                                          (212) 869-9741/8864
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                              unknown
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100.0%; Pr
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0.004;
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US-08-485-264A-114
Sequence 114, Application US/08485264A; Patent No. 6228983; GENERAL INFORMATION:
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                                                              RESULT 10
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; MOLECULE TYPE:
US-08-471-913A-114
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Matches
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                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PETTEWAY, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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ZIP: 10036-2711
                                                                                                          82 SLRSAHLAGO
                                                                                                                                                                                                                                                                               LENGTH: 25%
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Americas CITY: New York
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                                                                                                                                                                     Local Similarity
les 10; Conserv
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o. 6093794
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                                                                                                                                                                                                                                                                                                           254 amino acids
                                                                                                                                                                    66.7%; Score 10; llarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                unknown
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                                                                                                                                                                    Pred. No. 0.004;
Mismatches (
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APPLICANT: Bolognesi, Dani P.

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RESULT 11
US-08-474-349A-114
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Best Local S
Matches 10
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TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LAURA A.
REGISTRATION UNMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                          APPLICANT: Lambert, Deulls ...
APPLICANT: Petteway, Stephen R.
APPLICANT: Langicis, Alphonse J.
APPLICANT: Langicis, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION

"""""""" OF SEQUENCES: 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 66.7%; Score 10; Local Similarity 100.0%; Pred. No. 10; Conservative 0; Mismatci
               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 SLRSAHLAGQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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New York
                                                                                                                                                                                                   Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Pennie & Edmonds LLP
1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lambert, Dennis M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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0.004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-474-349A-114
                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEO ID NO: 114:
                                                                  Matches
                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
82 SLRSAHLAGO 91
                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                             TYPE: amino acid
                               1 SLRSAHLAGO 10
                                                                                                                                                                                                                            CENGTH:
                                                                  10;
                                                                                                                                                                                                                            254 amino acids
                                                                  Conservative
                                                                                   66.7%; Score 10; 100.0%; Pred. No.
                                                                    0;
                                                                                                                                                                                                                                                                                                                                                          7872-024
                                                                  Mismatches
                                                                                   DB 4; Length 254; 0.004;
                                                                    0,
                                                                  Indels
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                                                                  Gaps
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Search completed: January 28, 2003, 10:38:03 Job time: 23 secs

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RESULT 1
US-09-819-917-7
; Sequence 7, Application US/09819917
; Patent No. US2002004939A1
; GENERAL IMPORMATION:
GENERAL IMPORMATION:
APPLICANT: Fontana, Mariagrazia
APPLICANT: Giannelli, Valentina
APPLICANT: Rappuoli, Rina
TITLE OF INVENTION: Immunogenic Detoxified Mutants Of Cholera Toxin
FILE REFERENCE: CHIR0312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
CURRENT APPLICATION NUMBER: US/09/819,917
CURRENT FILING DATE: 2001-03-28
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15
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: //cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep: *
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: //cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep: *
: //cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *
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                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
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No matches found
                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    Query
Score Match Length DB
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Gapop 60.0 , Gapext 60.0
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(SIDSZ/gcgdata/geneseq/geneseqp-embl/AA198, DAT: *

(SIDSZ/gcgdata/geneseq/geneseqp-embl/AA199, DAT: *

(SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2000, DAT: *

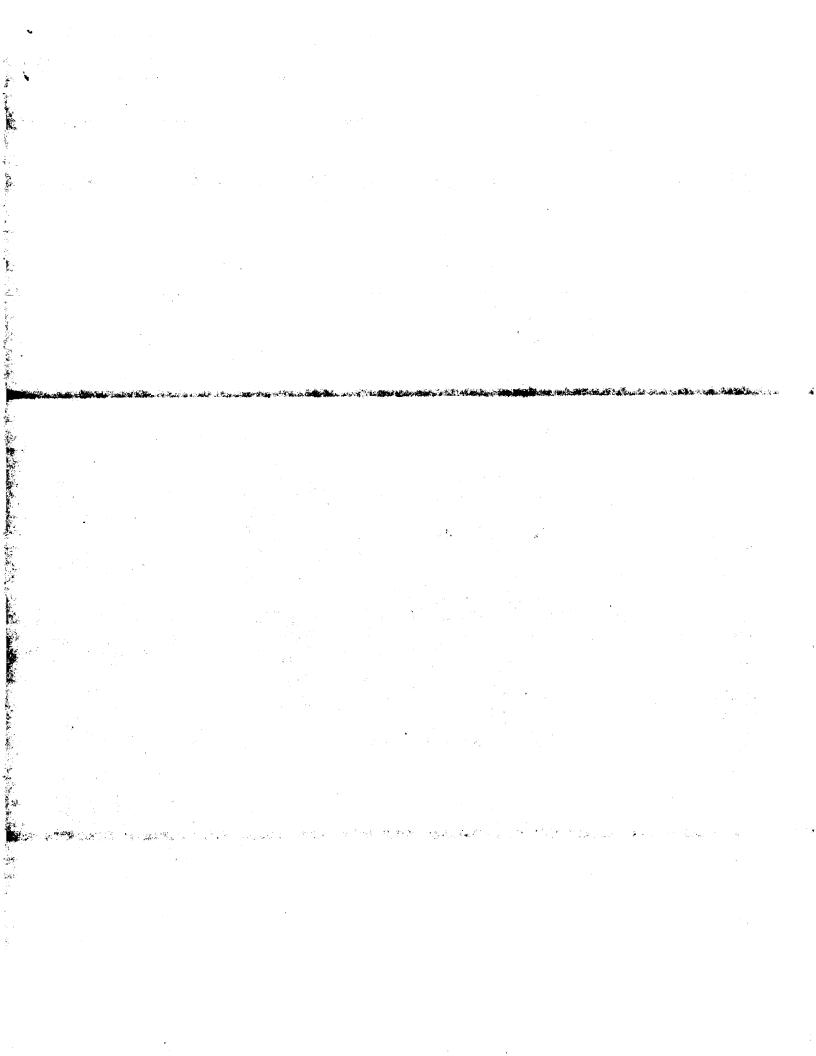
(SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001, DAT: *

(SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2001, DAT: *

(SIDSZ/gcgdata/geneseq/geneseqp-embl/AA2002, DAT: *

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
                                                                                       ID
                                                                                                                                                                                 SUMMARIES
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Search completed: January 28, 2003, 10:32:17 Job time : 127 secs



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Result
No.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                             APPLICANT: Domenighini, Mario
APPLICANT: Rappuoli, Rino
APPLICANT: Pizza, Mariagrazia
TITLE OF INVENTION: Immunogenic Detoxified Mutants of
TITLE OF INVENTION: Cholera Toxin and of the Toxin Lt, Their Preparation and
TITLE OF INVENTION: Their Use for the Preparation of Vaccines
NUMBER OF SEQUENCES: 41
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     STREET: 4560 Hort
CITY: Emeryville
STATE: California
                                                 COUNTRY: USA
ZIP: 94608-2916
                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score Match Length DB

    Application US/08823120
    6149919

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                                                                                       California
                                                                                                                                4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       January 28, 2003, 10:24:52 ; Search time 23 Seconds (without alignments)
19.189 Million cell updates/sec
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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Search completed: January 28, 2003, 10:38:03 Job time: 23 secs
                                                                                                                                                                                                                                    TELEFAX: (510) 601-2708

TELEFAX: (510 (655-3542)

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                     Best
                                                                                                                                       Matches
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/256

FILING DATE: 11-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: McClung, Barbara G.

REGISTRATION NUMBER: 33,113

REFERENCE/DOCKET NUMBER: 0315

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                6 VPNNKEFK 13
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186 VPNNKEFK 193
                                                                                                                                     Local Similarity 100 les 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                               53.3%; Scc
100.0%; Pr
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Pred. No. 0.11;
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US-09-819-917-5

Sequence 5, Application US/09819917

Sequence 5, Application US/09819917

Patent No. US20020044939A1

GENERAL INFORMATION:

APPLICANT: Pizza, Mariagrazia

APPLICANT: Fontana, Maria Rita

APPLICANT: Rappuoli, Rina

APPLICANT: Rappuoli, Rina

APPLICANT: Rappuoli, Rina

FILE OF INVENTION: Immunogenic Detoxified Mutants Of Cholera Toxin

FILE REFERENCE: CHIROJ12

CURRENT APPLICATION NUMBER: US/09/819,917

CURRENT FILING DATE: 2001-03-28
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No.
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Maximum DB seq length: 2000000000
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Perfect score:
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SEQ ID NO 5

LENGTH: 241

TYPE: PRT

ORGANISM: E. coli

US-09-819-917-5
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Search completed: January 28, 2003, 10:38:58 Job time: 13.3333 secs
                                                                                                            Matches
                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/981,208
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: 9513371.6
PRIOR FILING DATE: 1995-06-30
NUMBER OF SEQ ID NOS: 8
                                                      6 VPNNKEFK 13
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186 VPNNKEFK 193
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les 8; Conserv
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                                                                                                                       53.3%;
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Pred. No. 0.039;
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A;Molecule type: DNA
A;Residues: 1-259 <PIC>
A;Residues: 1-259 <PIC>
A;Residues: GB:M17894; NID:g146671; PIDN:AAA24093.1; PID:g146672
A;Note: the authors translated the codon TAT for residue 225 as Thr
C;Superfamily: heat-labile enterotoxin chain A
E;1-18/Domain: signal sequence #status predicted <SIG>
E;19-259/Product: heat-labile enterotoxin IIa chain A #status predicted <LTA>
                                                                                                                                                                                                                                                                  C;Accession: A29831
R;Pickett, C.L.; Weinstein, D.L.; Holmes, R.K.
J. Bacteriol. 169, 5180-5187, 1987
A;Title: Genetics of type IIa heat-labile enterotoxin of Escherichia coli: operon fusion A;Reference number: A91849; MUID:88032841; PMID:2822667
A;Accession: A29831
                                                                                                                                                                                                                                                                                                                                                                                                             heat-labile enterotoxin IIa chain A precursor - Escherichia coli
N;Alternate names: LT-IIa
C;Species: Escherichia coli
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
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Maximum DB seq length: 2000000000
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Perfect score:
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Query Match 60.0%; Score 9; DB 2; Ler Best Local Similarity 100.0%; Pred. No. 0.0056; Matches 9; Conservative 0; Mismatches 0;
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Copyright (c) 1993 - 2003 Compugen Ltd
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Search completed: January 28, 2003, 10:33:46 Job time : 25.6667 secs

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P13810;
                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE-88032841; PubMed=2822667;

MIEDILINE-88032841; PubMed=2822667;

Pickett C.L., Weinstein D.L., Holmes R.K.;

"Genetics of type IIa heat-labile enterotoxin of Escherichia coli:

"Genetics of type IIa heat-labile enterotoxin of Escherichia coli:

"Genetics of type IIa heat-labile enterotoxin of Escherichia coli:

"Genetics of type IIa heat-labile enterotoxin of Escherichia coli:

"Beacteriol. 169:5180-5187(1987).

"HE ACHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.

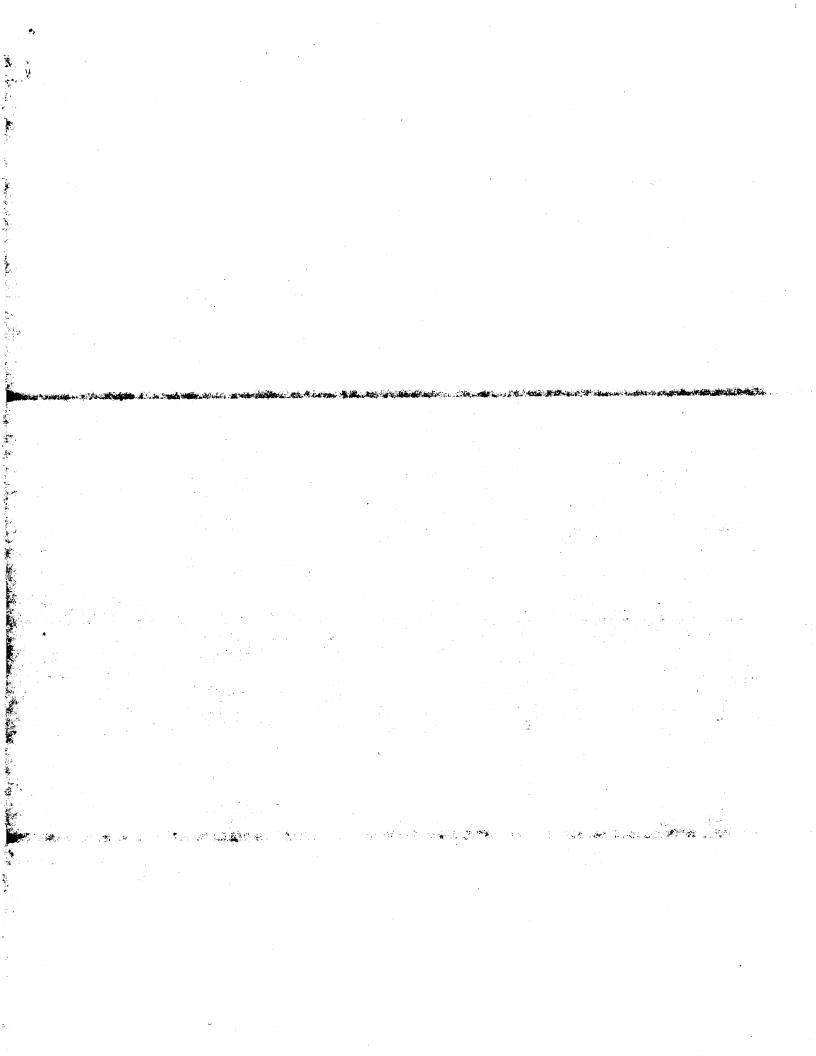
"HE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE."

"HE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE."

"HE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE."
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01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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Copyright (c) 1993 - 2003 Compugen Ltd
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(without alignments)
53.327 Million cell updates/sec
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    as its content
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Вb
                                                                                                                                                      Query Match 60.0
Best Local Similarity 100
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                  DISULFID ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001144; Enterotoxin_A.
Pfam; PF01375; Enterotoxin_A; 1.
PRINTS; PR00771; ENTEROTOXINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A29831; A29831.
HSSP; P43528; 1TII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterotoxin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M17894; AAA24093.1;
204 VPNNKEFKG
                                              6 VPNNKEFKG 14
                                                                                                                                                                                                                                                                                                                          203
128
259 /
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                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                  18
259
215
B
128
B
29242 MW;
                                                                                                                                                                                                60.0%;
                                                                                                                                                           0;
                                                                                                                                                      Score 9; DB 1; Pred. No. 0.0 0; Mismatches
                                                                                                                                                                                                                                                                                                                  HEAT-LABILE ENTEROTOXIN IIA, A CHAIN.
BY SIMILARITY.
BY SIMILARITY.
; 996F311A32CABEAA CRC64;
                                                                                                                                                                                                DB 1; I
5. 0.0021;
                                                                                                                                                                                                                                      Length 259
                                                                                                                                                           0
                                                                                                                                                           Indels
                                                                                                                                                           0;
                                                                                                                                                           Gaps
                                                                                                                                                           0
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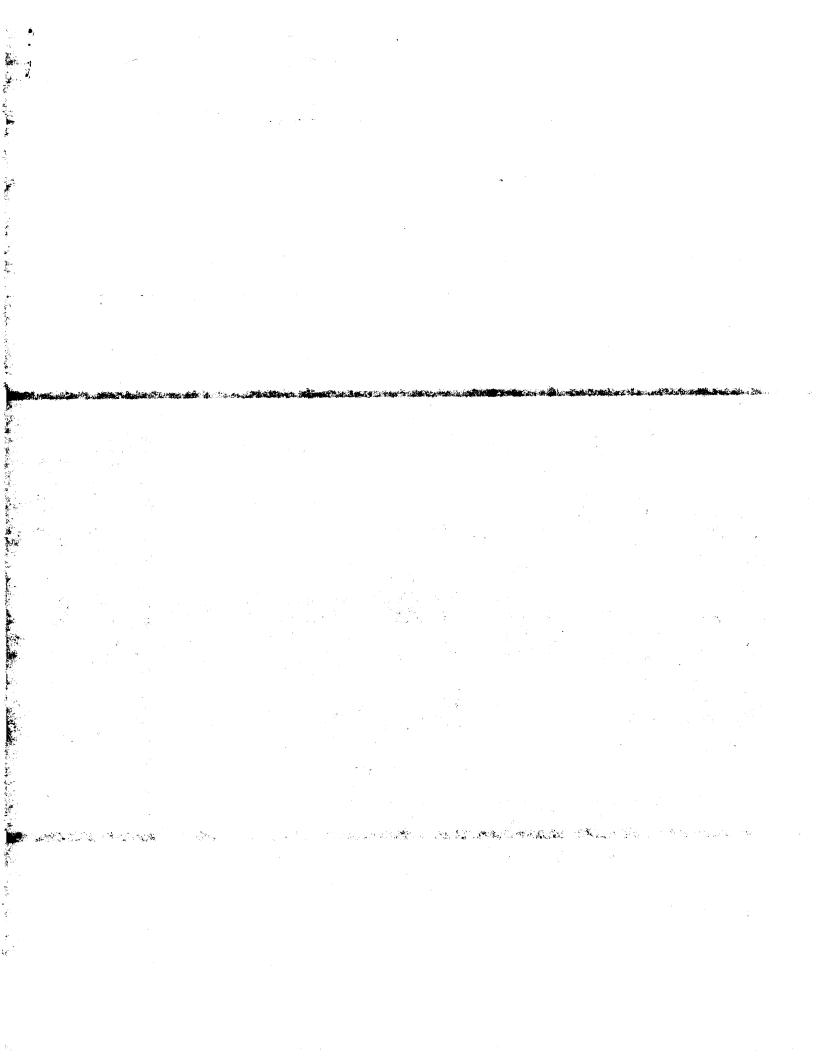
Search completed: January 28, 2003, 10:25:42 Job time: 11.6667 secs



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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 1000 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word size :
No matches found
                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                        Query
Score Match Length DB
                                                                                                                                                                            OLIGO
Gapop 60.0 , Gapext 60.0
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15
1 STFEQVPNNKEFKGV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671580 seqs, 206047115 residues
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sp_vident:*
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sp_bacteria:*
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sp_mammal:*
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                                                                                    SUMMARIES
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Search completed: January 28, 2003, 10:36:40 Job time: 53.333 secs



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Search completed: January 28, 2003, 10:32:17 Job time: 127 secs
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 1000 summaries
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                                                                                                                                        No matches found
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                                                                                                                                                                                                                                                                                                                                                                                                            and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                          Query
Score Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

11: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

12: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

13: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

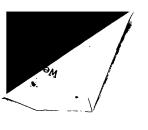
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

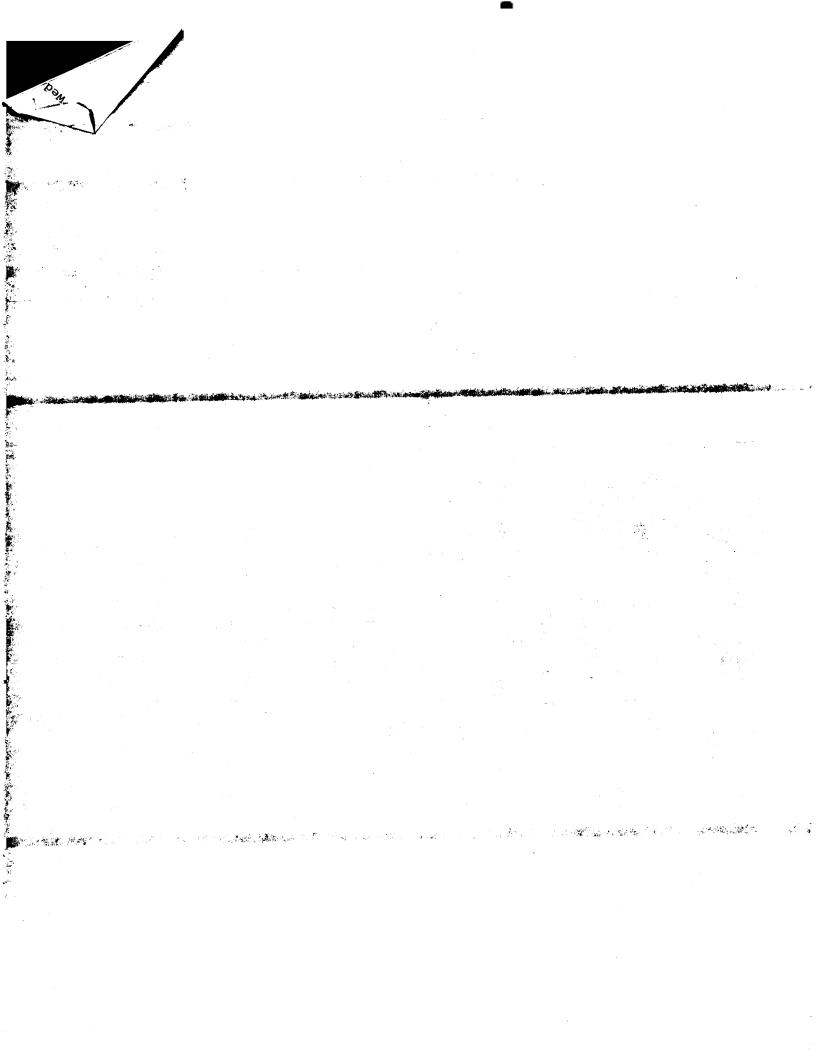
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 60.0 , Gapext 60.0
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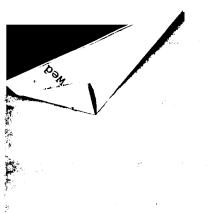
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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                      Result Query
No. Score Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table: OLIGO Gapop 60.0 , Gapext 60.0
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Search completed: January 28, 2003, 10:33:46 Job time: 24.6667 secs
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                                                                             No matches found
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                                                                                                                                                                                                                                                                                                                      PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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15
1 REFNSLPNNKASSDT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3 Compugen Ltd.
                                                                                                                                                                                                      SUMMARIES
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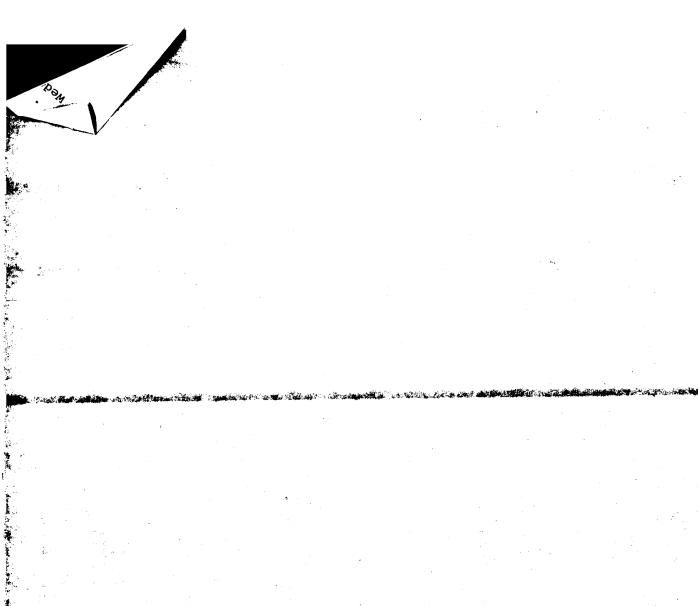
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Minimum DB
Maximum DB
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   Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E2BA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P43528;
01-NOV-1995
01-NOV-1995
15-JUN-2002
"Crystal structure of a new heat-labile enterotoxin, LT-IIb."; Structure 4:665-678(1996).
                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS). MEDLINE-96399713; PubMed-8805549;
                                                                                                                                                                                                             STRAIN-Isolate 41;
MEDLINE-89359131; PubMed=2670900;
MIEDLINE-89359131; PubMed=2670900;
Pickett C.L., Twiddy E.M., Coker C., Holmes R.K.;
Pickett C.L., Twiddy E.M., Pickett C.L., Fill Twide R.K.;
Pickett C.L., Twiddy E.M., Pickett C.L., Picke
                                                            van den Akker F., Sarfaty S., Hol W.G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat-labile enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E2BA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
enterotoxin IIB, A chain precursor (LT-IIB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.7
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                                                                                      Twiddy E.M., Connell T.D., Holmes R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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(without alignments)
53.327 Million cell updates/sec
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commendations are not the statement of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-1- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                            SEQUENCE
                                                                                                                                                                          CHAIN
                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                     Enterotoxin; Signal;
                                                                                                                                                                                                                  PRINTS; PR00771; ENTEROTOXINA
                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                     InterPro;
206 LPNNKASSDT 215
                             6 LPNNKASSDT 15
                                                                                                                                                                                                                                    PF01375; Enterotoxin_A; 1.
                                                                                                                                                                                                                                                   IPR001144; Enterotoxin_A.
                                                                                                                          263 AA;
                                                                                                                                          205
130
                                                            Conservative
                                                                                                                                         263
217
130
                                                                                                                          29485 MW; A56E8A069427CFB9 CRC64;
                                                                         66.7%;
                                                                                                                                                                                                       3D-structure.
                                                            0;
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Pred. No.
                                                                                                                                                                          HEAT-LABILE ENTEROTOXIN IIB, A CHAIN.
                                                              Mismatches
                                                                         DB 1; L, 0.00064;
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Search completed: January 28, 2003, 10:25:42 Job time: 11.6667 secs



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Result
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Search completed: January 28, 2003, 10:36:40 Job time: 53.333 secs
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Word size :
                                                           No matches found
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                                                                                                   Query
Score Match Length DB
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15
1 REFNSLPNNKASSDT 15
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1: sp_archea:
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sp_bacteria:*
sp_fungi:*
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sp_rvirus:*
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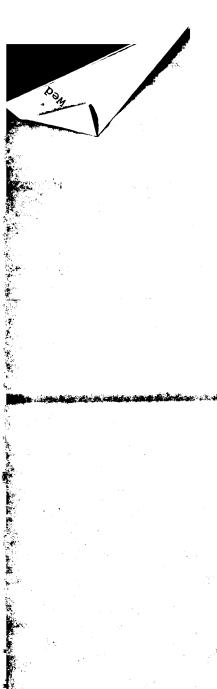
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No matches found
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1: /ggn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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19.189 Million cell updates/sec
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Search completed: January 28, 2003, 10:38:03 Job time: 23 secs



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Title:
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No matches found
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                                                                          Query
Score Match Length DB
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1: /cgn2_6/ptcdata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptcdata/2/pubpaa/PCTUS_PUBCOMB.pep:*

8: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*

10: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

15: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*

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17: /cgn2_6/ptcdata/2/pubpaa/US09_PUBCOMB.pep:*
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Gapop 60.0 , Gapext 60.0
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